

75185 .

**Delaval, Jan**

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**From:** Huynh, Phuong N.  
**Sent:** Monday, September 09, 2002 1:11 PM  
**To:** Delaval, Jan  
**Subject:** RE: 09/811,367

Jan,

Please search polypeptide of SEQ ID NO: 1 against commercial and interference databases.

Thanks,  
Neon  
Art unit 1644  
Mail 9E12  
Tel 308-4844

Jan Delaval  
Reference Librarian  
Biotechnology & Chemical Library  
CM1 1E07 - 703-308-4498  
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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 9, 2002, 14:54:46 ; Search time 16.41 Seconds  
(without alignments)  
1106.696 Million cell updates/sec

Title: US-09-811-367B-1

Perfect score: 1023

Sequence: 1 MDSVIYSMLPPTAQON.....GLQASCEVPLHGVCCKVRL 189

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	525.5	51.4	188	159421	mast cell function
2	201	19.6	225	138700	hNKR-p1a protein -
3	193	18.9	257	150146	gene 17.5 protein -
4	191	18.7	227	A46467	natural killer cel
5	190	18.6	233	PT0372	natural killer cel
6	182	17.8	231	PT0374	natural killer cel
7	180	17.6	216	PT0375	natural killer cel
8	178.5	17.4	240	154524	natural killer cel
9	176	17.2	244	A46274	HLV gp120-binding
10	175.5	17.2	223	A35917	NK-cell receptor p
11	174.5	17.1	304	JX0209	lectin, galactose/
12	174	17.0	139	JH0822	lymphocyte early a
13	169	16.5	237	UC7608	type II lectin-like
14	167	16.3	301	S13165	asialoglycoprotein
15	166	16.2	156	T28141	C type lectin, B1
16	165	16.1	284	S29855	asialoglycoprotein
17	164.5	16.1	306	A42230	lectin M-ASGP-BP p
18	162	15.8	262	A30573	T-cell surface gly
19	162	15.8	262	A45813	NKR-p1 protein hom
20	160.5	15.7	223	B46467	hepatic lectin 2 -
21	160.5	15.7	284	1LNRT1	hepatic lectin 2 -
22	160.5	15.7	301	1LNRT2	hepatic lectin H1
23	157.5	15.4	291	1LNHT1	natural killer cel
24	157	15.3	262	I49361	phospholipase-A(2)
25	156	15.2	1487	A48719	hepatic lectin hom
26	153.5	15.0	167	1WMVF2	Ly-49D-GE antigen
27	151.5	14.8	260	T149049	natural killer cel
28	149	14.6	170	T28140	NKR-p1 protein hom
29	148.5	14.5	220	C46467	

30	148.5	14.5	550	2	A28166	Kupffer cell recep
31	146.5	14.3	1326	2	B56395	secretory phosphol
32	146.5	14.3	1465	2	A56395	secretory phosphol
33	146	14.3	311	1	LNH02A	asialoglycoprotein
34	145.5	14.2	1479	2	T42710	mannose receptor,
35	143.5	14.0	144	2	PC7027	aggrelin alpha cha
36	142	13.9	146	2	JC7135	agglutinin beta
37	141.5	13.8	1458	1	A49707	phospholipase A2 r
38	140.5	13.7	267	2	I49053	Ly-49G.2 antigen
39	140.5	13.7	280	2	I49052	Ly-49G.1 antigen
40	139.5	13.6	3562	2	A47171	chondroitin sulfat
41	138.5	13.5	1463	2	A53210	pancreatic lipase A2 r
42	137.5	13.4	175	2	S29822	pancreatic stone p
43	137	13.4	165	2	A28351	pancreatic stone p
44	137	13.4	266	2	I49363	natural killer cel
45	137	13.4	742	2	JC7595	scavenger receptor

#### ALIGNMENTS

RESULT 1  
159421  
mast cell function associated antigen - rat  
C:Species: Rattus norvegicus (Norway rat)  
C>Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 05-Nov-1999  
R:Accession: 159421  
R:Guthmann, M.D.; Tal, M.; Pecht, I.  
Proc. Natl. Acad. Sci. U.S.A. 92, 9397-9401, 1995  
A>Title: A secretion inhibitory signal transduction molecule on mast cells is another  
A:Reference number: 159421; MUID:96016176  
A:Accession: 159421  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-188 <RES>  
A:Cross-references: EMBL:X79812; NID:g1020141; PIDN:CA56208.1; PID:g1020142  
A:Gene: mafa

Query Match 51.4%; Score 525.5; DB 2; Length 188;  
Best Local Similarity 53.5%; Pred. No. 4.6e-42;  
Matches 100; Conservative 29; Mismatches 57; Indels 1; Gaps 1;  
QY 1 MDSVIYSMLPPTAQONDYPOQSSSKPSCSLVAITLGLTAVLLSVLYTOWIL 60  
DB 1 MADNSITSTLELPAPRVQDDSRMKKAVLHRCVSYLVWVALGLTILMSLLYQRTL 60  
QY 61 CGSNSTICASCPCPDNRMKYGNHCYFVSVEKDMNSLFECLARDSHLVTDOEMS 120  
DB 61 CCGSGFMCSCSRCPNLMRMNGSHCYFSMEKRDWNSSLKFCADGSHLTFPPDQVNA 120  
QY 121 LLOVLEAFQWIGIRNNSGMRWEDGSPILNFSRISNSVYVQCGALNKGGLASCEVPL 180  
DB 121 LFQEVGEDFTWIGRLDIDGWRWEDGDPALSTS-ILSNVYVQCGTIRGGLASCEVAL 179  
QY 181 HGVCCKV 187  
DB 180 QWICEKV 186  
RESULT 2  
138700  
hNKR-p1a protein - human  
C:Species: Homo sapiens (man)  
C>Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 24-Sep-1999  
C:Accession: 138700  
R:Lanier, L.L.; Chang, C.; Phillips, J.H.  
J. Immunol. 153, 2417-2428, 1994  
A>Title: Human NKR-p1A: A disulfide-linked homodimer of the C-type lectin superfamily  
A:Reference number: 138700; MUID:94355407  
A:Accession: 138700  
A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA  
 A:Residues: 1-225 <RES>  
 A:Cross-references: EMBL:U11276; NID:g538270; PIDN:AAA21605.1; PID:g544496  
 C:Superfamily: natural killer cell receptor PI, C-type lectin homology  
 F:94-210/Domain: C-type lectin homology <LCH>

Query Match 19.6%; Score 201; DB 2; Length 225;  
 Best Local Similarity 26.0%; Pred. No. 1.7e-11;  
 Matches 58; Conservative 36; Mismatches 81; Indels 48; Gaps 8;

1 MNDVSIVSMLEFPTAQANDVGPQKSSSKP-----SCSCLVATTLG 44  
 1 MDQAIYAEILNLP-----DSGPSSSPSLPRDVCQSPHOFALKSCAGITLLVL- 53  
 45 LTLAVLLSVLLXOMILCOGSNSTCA-----SCSPCDPMKMYGNHCYFYS 90  
 54 VVTGLSVST-----SLQKSSIEKCSVDIQSNKKTPTERPGLNCPYWGQLREKCLFYS 109  
 91 VEKDMNSLEFLARDSHLVTTDQMSLQVFLSE--AFQWIGLR--NNSGWRWD 145  
 110 HTVNPNNSLADSTKESLLIRDEDLHTQNLIRDKAILFWIGLNFSLSEKMKMIN 169  
 146 GSPINFS--RISNSFVOTCGAINKNGLOASCEVPLHGVCCK 186  
 170 GSTLNSNDEIRDAKENSICISQTSVISEYCTEIRMICOK 212

RESULT 3  
 150146  
 gene 17.5 protein - chicken  
 C:Species: Gallus gallus (chicken)  
 C:Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 21-Jul-2000  
 C:Accession: 150146  
 R:Bernot, A.; Zoorob, R.; Auffray, C.  
 Immunogenetics 39, 221-229, 1994  
 A:Title: Linkage of a new member of the lectin supergene family to the chicken Mhc genes  
 A:Reference number: 150146; MVID:9416461  
 A:Accession: 150146  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-257 <BER>  
 A:Cross-references: GB:M88072; NID:g505324; PIDN:AAA8556.1; PID:g505325  
 C:Superfamily: C-type lectin homology  
 F:123-241/Domain: C-type lectin homology <LCH>

Query Match 18.9%; Score 193; DB 2; Length 257;  
 Best Local Similarity 26.6%; Pred. No. 1.1e-10;  
 Matches 49; Conservative 28; Mismatches 89; Indels 18; Gaps 4;

17 QAONDYGPQKSSSKSPSCSCL-----VAITGLTAVLLSVLLXOMILCOGSNSTC 69  
 64 EATTRGDEBERGQSGSELCRNRRVYLVALSAVPCULVALAVIYLGRPS---C 119  
 70 ASCPS---CPDRMKYGNHCYFYSVEKDMNSLEFLARDSHLVTTDQMSLQVFL 125  
 120 SRPSPSHVCPNMAVGFQGCYFSDTESDMNSRRECHRLGSLATLIDKEEFELQY 179  
 126 LSEAFICGLRNNSG---NRMEDGSPINFSRISNSFVOTCGAINKNGLOASCEVPL 182  
 180 QNRADWIGLHRAEGDEHNTWADGSAFTNRPVELKGGCAVLNGDGISALCHSEKFW 239  
 183 VCKK 186  
 240 VCSR 243

RESULT 4  
 A46467  
 natural killer cell receptor PI - mouse  
 N:Alternate names: NKR-PI protein  
 C:Species: Mus musculus (house mouse)

C:Date: 18-Jun-1993 #sequence\_revision 19-Feb-1999 #text\_change 05-May-2000  
 C:Accession: A46467; A46502; A46456  
 R:Giorda, R.; Trucco, M.  
 J. Immunol. 147, 1701-1708, 1991  
 A:Title: A family of genes selectively coexpressed in adherent lymphokine-activated K  
 A:Reference number: A46467; MVID:91349596  
 A:Accession: A46467

A:Molecule type: mRNA  
 A:Residues: 1-227 <GIO>  
 A:Cross-references: GB:M77676; NID:g200058  
 A:Experimental source: A-LAK cells, C57BL  
 A:Note: sequence extracted from NCBI backbone (NCBIN:52378, NCBIPI:52379); the sequenc  
 R:Giorda, R.; Welsberg, E.P.; Ip, T.K.; Trucco, M.  
 J. Immunol. 149, 1957-1963, 1992  
 A:Title: Genomic structure and strain-specific expression of the natural killer cell  
 A:Reference number: A46502; MVID:92388663  
 A:Accession: A46502

A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-109, 'H', 111-181, 'D', 183-227 <GI2>  
 A:Cross-references: GB:X64716; NID:g33395; PIDN:CAA45971.1; PID:g817989  
 A:Experimental source: BALB/c 3T3 fibroblastoid cell line  
 A:Note: sequence extracted from NCBI backbone (NCBIN:113037, NCBIN:113063, NCBIN:1130  
 J.Yokoyama, W.M.; Ryan, J.C.; Hunter, J.J.; Smith, H.R.; Stark, M.; Seaman, W.E.  
 J. Immunol. 147, 3229-3236, 1991

A:Title: CDNA cloning of mouse NKR-PI and genetic linkage with Lx-49. Identification  
 A:Reference number: A46456; MVID:92013158  
 A:Accession: A46456

A:Molecule type: mRNA  
 A:Residues: 1-38, 'L', 40-227 <XOK>

A:Cross-references: GB:M77753; NID:g198569; PIDN:AAA9366.1; PID:g198570  
 A:Note: sequence extracted from NCBI backbone (NCBIN:60429, NCBIPI:60431)  
 C:Superfamily: natural killer cell receptor PI, C-type lectin homology  
 F:94-210/Domain: C-type lectin homology <LCH>

Query Match 18.7%; Score 191; DB 2; Length 227;  
 Best Local Similarity 27.4%; Pred. No. 1.5e-10;  
 Matches 49; Conservative 43; Mismatches 71; Indels 16; Gaps 7;

24 POKSSSKSPSCSCLVATTLGL-TAVLLSVLLXO-----WILCOGS-NYST-CASCP 74  
 34 PRHSRLKLSLSCAGILLVYTLIGMSVYRLIQRPSIEKYVLIQENLNTTDCSALKE 93  
 75 CPDRMKYGNHCYFYSVEKDMNSLEFLARDSHLVTTDQMSLQVFLSEAF--CW 132  
 94 CPQDWLSHRDKCFHVSQVSTWEGLVDCDGKATMLIDQOEBLRFLLDSIKKYNFSF 153  
 133 IGUR---NNSGWRWEDSPINFS--RISNSFVOTCGAINKNGLOASCEVPLHGVCCK 186  
 154 IGLRYTLPLDMKMKWINSSTLNSDVLKITGTENDSCAASIDKVFESCSNDNRMICOK 212

RESULT 5  
 PT0372  
 natural killer cell receptor group 2, splice form A - human  
 N:Alternate names: NKG2-A; NKG2-B  
 N:Contents: Homo sapiens natural killer cell receptor group 2, splice form B  
 C:Species: Homo sapiens (man)  
 C:Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 05-May-2000  
 C:Accession: PT0372; MVID:91178434  
 R:Houchins, J.P.; Yabe, T.; McSherry, C.; Bach, F.H.  
 J. Exp. Med. 173, 1017-1020, 1991  
 A:Title: DNA sequence analysis of NKG2, a family of related CDNA clones encoding type  
 A:Reference number: PT0372; MVID:91178434  
 A:Accession: PT0372  
 A:Molecule type: mRNA  
 A:Residues: 1-233 <HOUI>  
 A:Cross-references: EMBL:X54867; NID:g35056; PIDN:CAA38649.1; PID:g35057  
 A:Experimental source: natural killer cell  
 A:Accession: PT0373  
 A:Molecule type: mRNA  
 A:Residues: 1-95, 114-233 <HOUI>

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A:Cross-references: GB:X54868; NID:g35058; PIDN:CA8650.1; PID:g35059
A:Experimental source: natural killer cell
C:Genetics:
A:Gene: GDB:KLRG1; NKG2
A:Cross-references: GDB:138773; OMIM:161555
A:Map position: 1pter-12pter
C:Superfamily: natural killer cell receptor PL; C-type lectin homology
C:Keywords: alternative splicing; glycoprotein; transmembrane protein
F:119-229/Domain: transmembrane #status predicted <TRA>
F:102,103,151,180/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:119-130,147-229,208-221/Disulfide bonds: #status predicted

Query Match      18.6%; Score 190; DB 2; Length 233;
Best Local Similarity 27.8%; Pred. No. 1.9e-10;
Matches 55; Conservative 35; Mismatches 86; Indels 22; Gaps 8;

OY 5 VIYSMELPFA7OQNNDYGPQOKSSSK--PSC-SCVAITTGILTAVALI----SVLYQ 57
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 38 IYYAELNLQKASQ---DFQGNDRKYHCKDLPAPREKLYIGILGIIILIMASVYTIYIP 94
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 58 WILCGSNST-----CASCPCPDPRMAYGNHCYFFSVEEKDNSSLFELCARDSL 110
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 95 SVLIQRHNNSSLMTRTQKARHCCHCPPEMITYSNCCYIGKERRRWEESILACTSKNSL 154
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 111 LVITDNOEMLLVFLSEAFQWIGL--RNSGMRWEDGSLNRS--ISSNPFOTGAIN 167
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 155 LVIDNEEKFLSIISPS--WIGVFRNSHHPWVTMNGLAFRHEIKDSDNAELNCAYIQ 212
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 168 KNGLASGCEVPPLHGVC 185
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 213 VNRLKSAQCGSSIIYHCK 230
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 6
PT0374
natural killer cell receptor group 2-C, splice form 1 - human
N:Alternate names: NKG-C
C:Species: Homo sapiens (man)
C:Date: 31-Mar-1992 #sequence, revision 31-Mar-1992 #text_change 19-May-2000
C:Accession: PT0374
R:Houchens, J.P.; Yabe, T.; McSherry, C.; Bach, F.H.
J. Exp. Med. 173, 1017-1020, 1991
A:Title: DNA sequence analysis of NKG2, a family of related cDNA clones encoding type II
A:Reference number: PT0372; MVID:91178434
A:Accession: PT0374
A:Molecule type: mRNA
A:Residues: 1-231 <HOU>
A:Cross-references: EMBL:X54869; NID:g35060; PIDN:CA8651.1; PID:g35061
A:Experimental source: natural killer cell
C:Genetics:
A:Gene: GDB:KLRG2; NKG2-C
A:Cross-references: GDB:9787095
A:Map position: 12p13-12p13
C:Superfamily: natural killer cell receptor PL; C-type lectin homology
C:Keywords: glycoprotein; transmembrane protein
F:71-96/Domain: transmembrane #status predicted <TRA>
F:27,100,149,178/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match      17.8%; Score 182; DB 2; Length 231;
Best Local Similarity 27.8%; Pred. No. 1.1e-09;
Matches 47; Conservative 32; Mismatches 76; Indels 14; Gaps 5;

OY 24 POKSSSKRPSGCLVAITGLTAVALISVLLYQWILCOGSNYST---CASCPCPDPRW 79
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 67 PEKLTAEVLGIICIV-----IMATVLTIVILPELFQNNSSPNRTQKARHCCHPEEW 121
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 80 KMYGNHCYFFSVEEKDNSSLFELCARDSLVLVITDNOEMLLVFLSAFCWIGL--RNN 138
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 122 IYVNSCYITGKRRRWEESILACTSKNSLISIDNEIKFLASILPS--WIGVFRNS 179
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |

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[illegible]

Db 122 ITYSNCTYIKERKTWEESLOACASKNSSSLSTIDNEEMFLSLIPSS--WIGVFNN 179  
QY 138 NSGWMEDGSPLNFSR--ISSNSFYOTCGAINKNGLOASSC 176  
Db 180 SSHHPWVTINGLAFKHEIKSDHAERNCAMLHVRLISDQC 220

RESULT 9  
A46274  
HIV gp120-binding C-type lectin - human  
C:Species: Homo sapiens (man)  
C:Date: 21-Sep-1993 #sequence\_revision 18-Nov-1994 #text\_change 01-Dec-1995  
C:Accession: A46274  
R:Curitis, B.M.; Schainowski, S.; Watson, A.J.  
Proc. Natl. Acad. Sci. U.S.A. 89, 8356-8360, 1992  
A:Title: Sequence and expression of a membrane-associated C-type lectin that exhibits CD  
A:Reference number: A46274; MUID:92390446  
A:Accession: A46274  
A:Status: preliminary  
A:Molecule type: nucleic acid  
A:Residues: 1-404 <CDR>  
A:Experimental source: placenta  
A:Note: sequence extracted from NCBI backbone (NCBIN:113134, NCBIPI:113135)  
F:256-377/Domain: C-type lectin homology <LCH>

Query Match 17.2%; Score 176; DB 2; Length 404;  
Best Local Similarity 30.7%; Pred. No. 6.9e-09;  
Matches 39; Conservative 23; Mismatches 53; Indels 12; Gaps 5;

QY 72 CPSCDPRMKTGNHCYFSVEEKDNSSLEFCLARDSHLVTIDNQMSLQVFLSEA-- 129  
Db 253 CHPEPWETFFQGNCFYFNSQNMHDSITACKVEGAQLVIKSAEQNFLQSSRSNR 312  
QY 130 FCWIGLR--NNSG-WRMEDGSPLN--NFSRI-----SSNSFYOTCGAINKNGLOASSCEVP 179  
Db 313 FTWMLSPLDNDBGTWQWVDGSPLPSPFOYNNRGNPEPNNVGEEDCAEFSSGNNMDKCNDA 372

QY 180 LHGVCK 186  
Db 373 KFWICK 379

RESULT 10  
A35917  
NK-cell receptor P1 - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 12-Apr-1991 #sequence\_revision 12-Apr-1991 #text\_change 24-Sep-1999  
C:Accession: A35917  
R:Giordano, R.; Rudert, W.A.; Vavassori, C.; Chambers, W.H.; Hiserodt, J.C.; Trucco, M.  
Science 249, 1298-1300, 1990  
A:Title: NKR-P1, a signal transduction molecule on natural killer cells.  
A:Reference number: A35917; MUID:90378305  
A:Accession: A35917  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-223 <GIO>  
A:Cross-references: GB:M62891; NID:g205722; PTDN:AAA41710.1; PID:g205723  
C:Superfamily: natural killer cell receptor P1; C-type lectin homology  
C:Keywords: transmembrane protein  
F:94-210/Domain: C-type lectin homology <LCH>

Query Match 17.2%; Score 175.5; DB 2; Length 223;  
Best Local Similarity 27.1%; Pred. No. 4.2e-09;  
Matches 49; Conservative 44; Mismatches 67; Indels 21; Gaps 9;

QY 24 FQKSSSKPSCSCLVATLGLT-TAVLLSVLYQ-----WILCOGSNYSTCASCPS-- 74  
Db 35 PRSHLALKLSGAGLILVALVGSILVRYVQKPSVPCRVLIQ-ENLSKTGS-PAKL 92

QY 75 -CPDRMKYGNHCYFSVEEKDNSSLEFCLARDSHLVTIDNQMSLQVFLSEA-- 130  
Db 93 KCPKDWLSHRDCFHVSYQFSITKTESLADCGGAGATLLVQDDELFNLTKRISSSF 152  
QY 131 CWIGLR--NNSGWMEDGSPLNFS--RISSNSFYOTCGAINKNGLOASSCEVP 185  
Db 153 -WIGLSYTLSDENMKWKNINSTLNSDVLSTIGDEKSCASVSQDKVLSKSCDSDNITWQC 211

QY 186 K 186  
Db 212 K 212

RESULT 11  
JX0209  
lectin, galactose/N-acetylglucosamine-specific - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 20-Aug-1999  
C:Accession: JX0209; PX0009  
R:Sato, M.; Kawakami, K.; Osawa, T.; Toyoshima, S.  
J. Biochem. 111, 331-336, 1992  
A:Title: Molecular cloning and expression of cDNA encoding a galactose/N-acetylglact  
A:Reference number: JX0209; MUID:92268032  
A:Accession: JX0209  
A:Molecule type: mRNA  
A:Residues: 1-304 <SAT>  
A:Cross-references: GB:S3676; NID:g249360; PTDN:AAB22171.1; PID:g249361  
R:Oda, S.; Sato, M.; Toyoshima, S.; Osawa, T.  
J. Biochem. 104, 600-605, 1988  
A:Title: Purification and characterization of a lectin-like molecule specific for gal  
A:Reference number: PX0009; MUID:89197865  
A:Accession: PX0009  
A:Molecule type: protein  
A:Residues: 102-120;137,'X',139-151 <ODA>  
C:Superfamily: hepatic lectin; C-type lectin homology  
C:Keywords: glycoprotein; lectin; macrophage; transmembrane protein  
F:173-296/Domain: C-type lectin homology <LCH>  
F:74,166/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 17.1%; Score 174.5; DB 2; Length 304;  
Best Local Similarity 27.5%; Pred. No. 7.1e-09;  
Matches 39; Conservative 27; Mismatches 61; Indels 15; Gaps 5;

QY 59 ILCOGSNYSTCAS-CPSCDPRMKTGNHCYFSVEEKDNSSLEFCLARDSHLVTIDNQ 117  
Db 156 LTCQLANLKNNGSEVACCPFLHWTEHSGCYWFSESEKSWPEADKCYRLNLSHLVNVNLSLE 215  
QY 118 ENSLQVFLSEAFQWIGLRNNSG-WRMEDGSPLN--NFSRISSNSFY-----QTCG 164  
Db 216 EONFLONRLANLVYVSWIDGDPNPFWRVDTGTFEKGFKWAPLQDPNWFGLGGEDCA 275

QY 165 AINKNG-LQASSCEVPLHGVC 185  
Db 276 HITGGFWNDVVCQRTFRWICE 297

RESULT 12  
JH0822  
lymphocyte early activation antigen AIM/CD69 - human  
C:Species: Homo sapiens (man)  
C:Date: 30-Sep-1993 #sequence\_revision 20-Aug-1994 #text\_change 08-Oct-1999  
C:Accession: JH0822; I56167; S60753  
R:Lopez-Cabrera, M.; Santis, A.G.; Fernandez-Ruiz, E.; Blacher, R.; Esch, F.; Sanchez  
J. Exp. Med. 178, 537-547, 1993  
A:Title: Molecular cloning, expression, and chromosomal localization of the human ear  
A:Reference number: JH0822; MUID:93340630  
A:Accession: JH0822  
A:Molecule type: mRNA  
A:Residues: 1-199 <LOP>  
A:Cross-references: GB:Z22576; NID:g397938; PTDN:CAA80298.1; PID:g397939

A:Note: the authors translated the codon CAA for residue 110 as Glu  
 R:Hamann, J.; Fiebig, H.; Strauss, M.  
 J. Immunol. 150, 4920-4927, 1993  
 A:Title: Expression cloning of the early activation antigen CD69, a type II integral mem  
 A:Reference number: 156167; MUID:93267093  
 A:Accession: 156167  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-199 <S>  
 A:Cross-references: GB:L07555; NID:g291897; PID:AB46359.1; PID:g291898  
 R:Sanlits, A.G.; Lopes-Cabreia, M.; Hamann, J.; Strauss, M.; Sanchez-Madrid, F.  
 Eur. J. Immunol. 24, 1692-1697, 1994  
 A:Title: Structure of the gene coding for the human early lymphocyte activation antigen  
 ceptors.  
 A:Reference number: S60753; MUID:94298875  
 A:Accession: S60753  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-199 <S>  
 A:Cross-references: EMBL:Z30426; NID:g525242; PID:CAA63017.1; PID:g558352  
 C:Comment: This protein is the earliest inducible cell surface glycoprotein expressed in  
 C:Genetics:  
 A:Gene: GDB:CD69  
 A:Cross-references: GDB:132925; OMIM:107273  
 A:Map position: 12p13-12p12  
 C:Superfamily: C-type lectin homology  
 C:Keywords: glycoprotein; phosphoprotein; receptor; transmembrane protein  
 F:38-66/Domain: transmembrane #status predicted <TM>  
 F:85-194/Domain: C-type lectin homology <LCH>  
 F:18,30/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted  
 F:31/Binding site: phosphate (Thr) (covalent) (by casein kinase II) #status predicted  
 F:166/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 17.0%; Score 174; DB 2; Length 199;  
 Best Local Similarity 22.9%; Pred. No. 5.2e-09;  
 Matches 40; Conservative 33; Mismatches 76; Indels 26; Gaps 5;

QY 30 SSRKSCGLVATITGLTRAVLLSVLYLWILCOGSSNYSTCASC-----SC 75  
 DB 30 STRHSGFOYVPLCAVMNVFITTILIALLSVGOY---NCPQYTFSPMSDSHVSQC 85  
 QY 76 PDRMRKGNHGYFSEVEKDMNNSLEFCLARDSHLVITDNOEMSLLOVFLSEAFQWIGL 135  
 DB 86 SEDWVGQKRCYFTSTYKRSFSAONACSEHGATLAVIDSEKDMFLKRYAREEHWVGL 145  
 QY 136 RNSG--WRWEDGSPLN--FSRISNSFEVOTCGAINKGLQASSCEVPLHGVCKR 186  
 DB 146 KKEGHPMKWMSNGKEFNMFVVTGSDK---CVFLKTEVSSMECEKNLYWICNK 196

RESULT 13  
 JC7608  
 type II lectin-like immunoreceptor - human  
 C:Species: Homo sapiens (man)  
 C:Date: 30-Jun-2001 #sequence\_revision 30-Jun-2001 #text\_change 30-Jun-2001  
 C:Accession: JC7608  
 R:Hamann, J.; Fiebig, H.; Strauss, M.; Hamann, J.; Strauss, M.; Sanchez-Madrid, F.  
 Eur. J. Immunol. 24, 1692-1697, 1994  
 A:Title: Expression cloning of the early activation antigen CD69, a type II integral mem  
 A:Reference number: 156167; MUID:93267093  
 A:Accession: 156167  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-199 <S>  
 A:Cross-references: GB:L07555; NID:g291897; PID:AB46359.1; PID:g291898  
 R:Sanlits, A.G.; Lopes-Cabreia, M.; Hamann, J.; Strauss, M.; Sanchez-Madrid, F.  
 Eur. J. Immunol. 24, 1692-1697, 1994  
 A:Title: Structure of the gene coding for the human early lymphocyte activation antigen  
 ceptors.  
 A:Reference number: S60753; MUID:94298875  
 A:Accession: S60753  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-199 <S>  
 A:Cross-references: EMBL:Z30426; NID:g525242; PID:CAA63017.1; PID:g558352  
 C:Comment: This protein is the earliest inducible cell surface glycoprotein expressed in  
 C:Genetics:  
 A:Gene: GDB:CD69  
 A:Cross-references: GDB:132925; OMIM:107273  
 A:Map position: 12p13-12p12  
 C:Superfamily: C-type lectin homology  
 C:Keywords: glycoprotein; phosphoprotein; receptor; transmembrane protein  
 F:38-66/Domain: transmembrane #status predicted <TM>  
 F:85-194/Domain: C-type lectin homology <LCH>  
 F:18,30/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted  
 F:31/Binding site: phosphate (Thr) (covalent) (by casein kinase II) #status predicted  
 F:166/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 16.5%; Score 169; DB 2; Length 237;  
 Best Local Similarity 21.6%; Pred. No. 1.8e-08;  
 Matches 52; Conservative 39; Mismatches 92; Indels 58; Gaps 9;

QY 1 MTDVSIYMLEL-----PTAQOANDYQPOQSSSKRSCGLVATITGLTRAVL 50  
 DB 1 MTSSEITAAVRFRKNERKSSGINTMSSAASKERAPLKSNTGFFKLKALIFELLALS 60  
 QY 51 LSV-----LLYQWILCOGSSNY---STCASCSPCDPRMKYGNHCY 87  
 DB 61 FPIAEVIFPQKYSOLLEKKTETKELVTTLECYKKNMPVEETAMSC--CPKRMKSFSSNCY 118  
 QY 88 YPSVEKDMNNSLEFCLARDSHLVITDNOEMSLLOVFLSEAFQWIGLRLNNSG---WRW 143  
 DB 119 FISTESASQWDEKDKARNEAHLLVINTQEBDFITQNLQESAIYVGLSDPEQGRHWQ 178  
 QY 144 EDGSPLEFSRISNSP-----VOTCGAIN-----KGLQASSCEVPLHGVCKR 188  
 DB 179 VQQTPTN---SSFTFHPHREPSDPRNERCVLNFRRKSPKRMGNDVNCIGPORSVCEMMK 234  
 QY 189 L 189  
 DB 235 I 235

RESULT 14  
 S13165  
 asialoglycoprotein receptor - mouse  
 N:Alternate names: hepatic lectin  
 C:Species: Mus musculus (house mouse)  
 C:Date: 21-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 20-Aug-1999  
 C:Accession: S13165  
 R:Sanford, J.P.; Doyle, D.  
 Biochim. Biophys. Acta 1087, 259-261, 1990  
 A:Title: Mouse asialoglycoprotein receptor cDNA sequence: conservation of receptor ge  
 A:Reference number: S13165; MUID:91027942  
 A:Accession: S13165  
 A:Molecule type: mRNA  
 A:Residues: 1-301 <S>  
 A:Cross-references: EMBL:X53042; NID:g53104; PID:CAA37211.1; PID:g53105  
 C:Superfamily: hepatic lectin; C-type lectin homology  
 C:Keywords: glycoprotein; liver; transmembrane protein  
 F:170-293/Domain: C-type lectin homology <LCH>

Query Match 16.3%; Score 167; DB 2; Length 301;  
 Best Local Similarity 25.9%; Pred. No. 3.6e-08;  
 Matches 55; Conservative 29; Mismatches 72; Indels 56; Gaps 9;

QY 27 KSSSKRSCGLVATITGLTRAVLL-----SVLLY----- 56  
 DB 92 KETFSNFSSSTLMRGALDTLGGSTNAIITSMIAOLEKQOOLKADHSTLLFLKHFPM 151  
 QY 57 -OMILCO---GSNYSTCASCSPCDPRMKYGNHCYFSEVEKDMNNSLEFCLARDSHLL 111  
 DB 132 LRTITCOLAIPYPSNGTEC-----CPVNWYFEGSCGWFPSRDGLTAEADQYCOLLENHLL 206  
 QY 112 VITDNOEMSLLOVFLSEAFQWIGLRLNNSG--WRWEDGSPLEFSRISNSFVQ----- 161  
 DB 207 VINSREDOQFVVKHRSQFHWIGLITDRDGSWMKWDCTDTR-SNYRMWAFQPDNMQGHQ 265  
 QY 162 ---TCGAINKNG-LQASSCEVPLHGVCKR 188  
 DB 266 GGEDCAETLSDGHMNDNFCQOVNRMVCEKR 297

RESULT 15  
 T28141  
 C type lectin, B locus - chicken  
 C:Species: Gallus gallus (chicken)  
 C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
 C:Accession: T28141



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 9, 2002, 15:00:06 : Search time 11.9 seconds

(without alignments)  
614,958 Million cell updates/sec

Title: US-09-811-367b-1

Perfect score: 1023

Sequence: 1 MTDSEVYSMELPTATQAN.....GLQSSCEVPLHGVCCKVRL 189.

Scoring table: BIOSUM62

Gapop 10.0, Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	196.5	19.2	179	1	CD94_HUMAN
2	196.5	19.2	199	1	CD69_MOUSE
3	191	18.7	227	1	NK11_MOUSE
4	190	18.6	233	1	NKGA_HUMAN
5	186	18.2	231	1	NKGD_HUMAN
6	180	17.6	216	1	NKGE_HUMAN
7	178.5	17.4	240	1	NKGI_HUMAN
8	175.5	17.2	223	1	NK13_RAT
9	174.5	17.1	304	1	MMGL_MOUSE
10	174	17.0	199	1	CD69_HUMAN
11	168	16.4	149	1	LEC1_HUMAN
12	167	16.3	301	1	LEC1_MOUSE
13	164.5	16.1	306	1	MMGL_RAT
14	163.5	16.0	283	1	LEC1_MOUSE
15	162	15.8	262	1	LY4A_MOUSE
16	160.5	15.7	223	1	NK12_MOUSE
17	160.5	15.7	283	1	LEC1_RAT
18	157.5	15.4	290	1	LEC1_HUMAN
19	156.5	15.3	163	1	V339_FOWPY
20	156.5	15.3	167	1	LEC1_RAT
21	153.5	15.0	167	1	V008_FOWPY
22	151.5	14.8	263	1	NK14_MOUSE
23	148.5	14.5	220	1	NK14_MOUSE
24	148.5	14.5	550	1	KCCR_RAT
25	147.5	14.4	175	1	PGCG_HUMAN
26	147	14.4	174	1	PAP3_MOUSE
27	146.5	14.3	548	1	KCCR_MOUSE
28	146	14.3	311	1	LEC1_HUMAN
29	141.5	13.8	1458	1	PA2R_RABIT
30	140.5	13.7	280	1	KLR7_MOUSE
31	139.5	13.6	3562	1	PGCV_CHICK
32	138.5	13.5	1463	1	PA2R_BOVIN
33	137.5	13.4	175	1	PAP1_MOUSE

34	137	13.4	165	1	LITH_RAT	P10758	rattus norv
35	136.5	13.3	321	1	FCE2_HUMAN	P06734	homo sapien
36	136.5	13.3	331	1	FCE2_MOUSE	P20693	mus musculus
37	136	13.3	163	1	AMP_HEMAM	P05140	hemipter
38	136	13.3	266	1	KLR3_MOUSE	O64329	mus musculus
39	134.5	13.1	175	1	LITH_BOVIN	P23132	bos taurus
40	134.5	13.1	175	1	PAP2_MOUSE	O09037	mus musculus
41	134	13.1	207	1	LEC1_MOUSE	P07207	gallus galli
42	133.5	13.0	2109	1	PGCA_CHICK	P07898	gallus galli
43	132.5	13.0	175	1	PAP1_RAT	P25031	rattus norv
44	131.5	12.9	2333	1	PGCA_CANFA	O28343	canis faml
45	131.5	12.9	2415	1	PGCA_HUMAN	P16112	homo sapien

## ALIGNMENTS

RESULT 1  
CD94\_HUMAN STANDARD; PRT: 179 AA.  
ID Q13241;  
AC 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE Natural killer cells antigen CD94 (KP43) (killer cell lectin-like  
DE receptor subfamily D, member 1).  
GN KLRD1 OR CD94.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Blood;  
RX MEDLINE=96011848; PubMed=7589107;  
RA Chang C., Rodriguez A., Carretero M., Lopez-Botet M., Phillips J.H.,  
R Lanier L.L.;  
RT "Molecular characterization of human CD94: a type II membrane  
RT glycoprotein related to the C-type lectin superfamily.";  
RL Eur. J. Immunol. 25:2433-2437(1995).  
CC -1- FUNCTION: PLAYS A ROLE AS A RECEPTOR FOR THE RECOGNITION OF MHC  
CC CLASS I HLA-E MOLECULES BY NK CELLS AND SOME CYTOTOXIC T-CELLS.  
CC -1- SUBUNIT: CAN FORM DISULFIDE-BONDED HETERODIMER WITH NKG2 FAMILY  
CC MEMBERS.  
CC -1- SUBCELLULAR LOCATION: Type II membrane protein.  
CC -1- TISSUE SPECIFICITY: NATURAL KILLER CELLS.  
CC -1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.  
CC -1- DATABASE: NAME=PROW; NOME=CD guide CD94 entry;  
CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd94.htm".  
CC  
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CC  
CC EMBL: U30610; AAC50291.1; -  
CC MIM: 602894; -  
CC InterPro: IPR001304; lectin\_c.  
CC Pfam: PF00059; lectin\_c; 1.  
CC SMART: SM00034; CLECT; 1.  
CC PROSITE: PS00615; C-TYPE\_LLECTIN\_1; FALSE\_NEG.  
CC PROSITE: PS50041; C-TYPE\_LLECTIN\_2; 1.  
KW Antigen; Receptor; Glycoprotein; Transmembrane; Signal-anchor; Lectin.  
FT DOMAIN 1 10 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 11 31 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)  
FT FT  
FT DOMAIN 32 179 EXTRACELLULAR (POTENTIAL).  
FT FT 98 C-TYPE LECTIN (LONG FORM).  
FT FT 61 BY SIMILARITY.  
FT FT 72 BY SIMILARITY.  
FT DISULFID 89 174  
FT DISULFID 89 174



CC -1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.  
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 CC  
 DR EMBL: M77676; AAA38822.1; -  
 DR EMBL: M77753; AAA39366.1; -  
 DR MGD: MG1:107540; LY55a.  
 DR InterPro: IPR001304; lectin\_c.  
 DR Pfam: PF000059; lectin\_c.1.  
 DR SMART: SM00034; CLECT.1.  
 DR PROSITE: PS00615; C-TYPE-LECTIN\_1; FALSE\_NEG.  
 DR PROSITE: PS50041; C-TYPE-LECTIN\_2; 1.  
 DR GlycoProtein; Antigen; Transmembrane; Signal-anchor; Lectin.  
 KW DOMAIN 1 42 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 43 62 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)  
 FT (POTENTIAL).  
 FT DOMAIN 63 227 EXTRACELLULAR (POTENTIAL).  
 FT DISULFID 93 212 C-TYPE LECTIN (LONG FORM).  
 FT DISULFID 94 105 BY SIMILARITY.  
 FT DISULFID 122 210 BY SIMILARITY.  
 FT CARBOHYD 189 202 BY SIMILARITY.  
 FT CARBOHYD 83 83 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 169 169 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CONFLICT 39 39 S -> L (IN REF. 2).  
 SQ SEQUENCE 227 AA; 25689 MW; 0599A2587DF0B615 CRC64;  
 Query Match 18.7%; Score 191; DB 1; Length 227;  
 Best Local Similarity 27.4%; Pred. No. 4.2e-11;  
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 QY 24 POKSSSKRPSCLVAITGLT-TAVLSVLVLYO-----WILCOGS-NYST-CASCPS 74  
 DB 34 PRHRRAALKSLSCGLILVLTILGMSVLVRLVLOKPEIECYLIQENLNTYDSCAKLE 93  
 QY 75 CPDRMKYGHNYCYFVEEKDNMSSEFLCARSLSHLVITDNOEMSLQVFLSEAF--CW 132  
 DB 94 CPQDWLSHRDKCHVSVQSVNTMEGLVDCGKATMLIDODERLRLDSIKRYSPFW 153  
 QY 133 IGLR---NNSGWRWEGSPINFE--RISNSFYQTCGAINKNGLOASSCEVPLHGVCKR 186  
 DB 154 IGLRYLPLDMNMKWMINGSTLNSDLKITGDTENDSCAAGSDKVTFCNSDNRMICOK 212  
 RESULT 4  
 NKG2A\_HUMAN STANDARD; PRT; 233 AA.  
 AC P26715;  
 DT 01-AUG-1992 (Rel. 23, Created)  
 DT 01-AUG-1992 (Rel. 23, Last sequence update)  
 DT 01-MAR-2002 (Rel. 41, Last annotation update)  
 DE NKG2-A/NKG2-B type II integral membrane protein (NKG2-A/B activating  
 DE NK receptor).  
 GN KLRK1 OR NKG2A.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-91178434; PubMed-2007850;  
 RA Houchins J.P., Yabe T., McSherry C., Bach F.H.;  
 RT "DNA sequence analysis of NKG2, a family of related cDNA clones  
 RT encoding type II integral membrane proteins on human natural killer  
 RT cells".  
 RL J. Exp. Med. 173:1017-1020(1991).

RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-96337918; PubMed-8753859;  
 RA Plougastel B., Jones T., Trowsdale J.;  
 RT "Genomic structure, chromosome location, and alternative splicing of  
 RT the human NKG2A gene".  
 RL Immunogenetics 44:286-291(1996).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-98260668; PubMed-9598306;  
 RA Plougastel B., Trowsdale J.;  
 RT "Sequence analysis of a 62-kb region overlapping the human KLRK  
 RT cluster of genes".  
 RL Genomics 49:193-196(1998).  
 CC -1- FUNCTION: PLAYS A ROLE AS A RECEPTOR FOR THE RECOGNITION OF MHC  
 CC CLASS I HLA-E MOLECULES BY NK CELLS AND SOME CYTOTOXIC T-CELLS.  
 CC -1- SUBUNIT: CAN FORM DISULFIDE-BONDED HETERODIMER WITH CD94.  
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein.  
 CC -1- ALTERNATIVE PRODUCTS: THE NKG2-A AND -B PEPTIDES APPEAR TO BE  
 CC -1- TISSUE SPECIFICITY: NATURAL KILLER CELLS.  
 CC -1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.  
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 CC  
 DR EMBL: X54867; CA38649.1; -  
 DR EMBL: X54868; CA38650.1; -  
 DR EMBL: U54786; AAB17133.1; -  
 DR EMBL: U54783; AAB17133.1; JOINED.  
 DR EMBL: U54784; AAB17133.1; JOINED.  
 DR EMBL: U54785; AAB17133.1; JOINED.  
 DR EMBL: AF023840; AAC17488.1; -  
 DR PIR: P03722; P03732.  
 DR PIR: P03733; P03733.  
 DR HSSP: P16581; IEST.  
 DR MIM: 161555; -  
 DR InterPro: IPR001304; lectin\_c.  
 DR Pfam: PF000059; lectin\_c.1.  
 DR SMART: SM00034; CLECT.1.  
 DR PROSITE: PS00615; C-TYPE-LECTIN\_1; FALSE\_NEG.  
 DR PROSITE: PS50041; C-TYPE-LECTIN\_2; 1.  
 KW Receptor; Transmembrane; Multigene family; Signal-anchor; Lectin;  
 KW Glycoprotein; Alternative splicing  
 FT DOMAIN 1 70 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 71 93 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)  
 FT (POTENTIAL).  
 FT DOMAIN 94 233 EXTRACELLULAR (POTENTIAL).  
 FT DISULFID 118 231 C-TYPE LECTIN (LONG FORM).  
 FT DISULFID 119 130 BY SIMILARITY.  
 FT DISULFID 147 229 BY SIMILARITY.  
 FT DISULFID 208 221 BY SIMILARITY.  
 FT CARBOHYD 102 102 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 103 103 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 151 151 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 180 180 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT VARSPLIC 96 113 MISSING (IN ISOFORM NKG2-B).  
 SQ SEQUENCE 233 AA; 26287 MW; 1654BD7958C81A84 CRC64;  
 Query Match 18.6%; Score 190; DB 1; Length 233;  
 Best Local Similarity 27.8%; Pred. No. 5.4e-11;  
 Matches 55; Conservative 35; Mismatches 86; Indels 22; Gaps 8;  
 QY 5 VIYSMLPLPATOANDYGPQKSSSK--PSC--SCVAITLGLTAVLT-----SVLLYQ 57  
 DB 38 IYIAELNLQKASQ---DFQGNDRKYHCKDLPSPAEKLVIGLIGLILCLIMASVYTIWIP 94

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QY 58 WILCOGNSYST-----CASCPCSPDRMKYGNHCYFVSVEKDNSSLFELCARDSL 110
DB 95 STLIQRNNSLNTRTOKARHCHGCHPEWITYSNCTYIGKERETWESLLACTSKNSL 154
QY 111 LVITDQEMSLQVLEAFWICGL-RNNSGWRWEDGSPLEFSR--ISSNFPVOTCGAIN 167
DB 155 LSLDNEEMKFLSISPPS--WIGVFRNSSHHPPVTMNGLAFKHEINDSDAELNCANVLQ 212
QY 168 KNGLOASSCEVPLHGVCK 185
DB 213 VNRLKSAQCGSSIIYHCK 230

RESULT 5
NKGC_HUMAN STANDARD; PRT; 231 AA.
ID P26717; Q43802;
AC 01-AUG-1992 (Rel. 23, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DE 01-MAR-2002 (Rel. 41, Last annotation update)
DE NKG2-C type II integral membrane protein (NKG2-C activating NK
DE receptor).
GN KIR2C OR NKG2C.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606; [1]
RN RP SEQUENCE FROM N.A.
RX MEDLINE=91178434; PubMed=2007850;
RA Houchins J.P., Yabe T., McSherry C., Bach F.H.;
RT "DNA sequence analysis of NKG2, a family of related cDNA clones
RT encoding type II integral membrane proteins on human natural killer
RT cells.";
RL J. Exp. Med. 173:1017-1020(1991). [2]
RN RP SEQUENCE FROM N.A.
RX MEDLINE=98350122; PubMed=9683661;
RA Glienke J., Sobanov Y., Brostjan C., Steffens C., Nguyen C.,
RA Lehnrich H., Hofer E., Francis F.;
RT "The genomic organization of NKG2C, E, F, and D receptor genes in the
RT human natural killer gene complex.";
RL Immunogenetics 48:163-173(1998). [3]
RN RP SEQUENCE FROM N.A.
RC TISSUE=Lymphoid;
RA Blasson R.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases
CC -1- FUNCTION: PLAYS A ROLE AS A RECEPTOR FOR THE RECOGNITION OF MHC
CC CLASS I HLA-E MOLECULES BY NK CELLS AND SOME CYTOTOXIC T-CELLS.
CC -1- SUBUNIT: CAN FORM DISULFIDE-BONDED HETERODIMER WITH CD94.
CC -1- SUBCELLULAR LOCATION: TYPE II membrane protein.
CC -1- TISSUE SPECIFICITY: NATURAL KILLER CELLS.
CC -1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: X54869; CAA38651.1; -
CC EMBL: AJ001684; CA004922.1; -
CC EMBL: Y13055; CAA73498.1; -
CC FTR: P70374; P70374.
CC MIM: 602891; -
CC InterPro: IPR001304; lectin.c.
CC Pfam: PF000059; lectin.c; 1.
CC SMART: SM00034; LECTC; 1.
CC PROSITE: PS00615; C_TYPE_LECTIN_1; FALSE_NEG.
CC PROSITE: PS50041; C_TYPE_LECTIN_2; 1.

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KW Receptor; Transmembrane; Multigene family; Signal-anchor; Lectin;
KM Glycoprotein.
FT DOMAIN 1 70 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 71 93 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT DOMAIN 94 231 (POTENTIAL).
FT DOMAIN 116 229 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 117 128 C-TYPE LECTIN (LONG FORM).
FT DISULFID 145 227 BY SIMILARITY.
FT DISULFID 206 219 BY SIMILARITY.
FT CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 149 149 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 178 178 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 161 161 M->I (IN REF. 1).
SQ SEQUENCE 231 AA; 26072 MW; 6B971EECD7542930 CRC64;

Query Match 18.2% Score 186; DB 1; Length 231;
Best Local Similarity 28.4%; Pred. No. 1.3e-10;
Matches 48; Conservative 31; Mismatches 76; Indels 14; Gaps 5;

QY 24 PQQRSSSKPSCSLVAITGLLAVLLSVLYOMILCOGNSYST---CASCPCSPDRW 79
DB 67 PPEKTLAEVLGIICIV-----LMAVTLKTYILIPLEQNNSSPNRTQKARHCHGCHPEM 121
QY 80 MKYGNHCYFVSVEKDNSSLFELCARDSLIVITDQEMSLQVLEAFWICGL-RNN 138
DB 122 IYNSNCYIGKERETWESLLACTSKNSLSLIDNEEMKFLASILPSS--WIGVFRNS 179
QY 139 SGWRWEDGSPLEFSR--ISSNFPVOTCGAINKNGLOASSCEVPLHGVCK 185
DB 180 SHHPVVTINGLAFKHKIKDSDAELNCANVLOYNRLKSAQCGSSMIYHCK 228

RESULT 6
NKGD_HUMAN STANDARD; PRT; 216 AA.
ID P26718;
AC 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE NKG2-D type II integral membrane protein (NKG2-D activating NK
DE receptor).
GN KIR2D OR NKG2D.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606; [1]
RN RP SEQUENCE FROM N.A.
RX MEDLINE=91178434; PubMed=2007850;
RA Houchins J.P., Yabe T., McSherry C., Bach F.H.;
RT "DNA sequence analysis of NKG2, a family of related cDNA clones
RT encoding type II integral membrane proteins on human natural killer
RT cells.";
RL J. Exp. Med. 173:1017-1020(1991). [2]
RN RP SEQUENCE FROM N.A.
RX MEDLINE=98350122; PubMed=9683661;
RA Glienke J., Sobanov Y., Brostjan C., Steffens C., Nguyen C.,
RA Lehnrich H., Hofer E., Francis F.;
RT "The genomic organization of NKG2C, E, F, and D receptor genes in the
RT human natural killer gene complex.";
RL Immunogenetics 48:163-173(1998).
CC -1- FUNCTION: PLAYS A ROLE AS A RECEPTOR FOR THE RECOGNITION OF MHC
CC CLASS I HLA-E MOLECULES BY NK CELLS AND SOME CYTOTOXIC T-CELLS.
CC -1- SUBUNIT: CAN FORM DISULFIDE-BONDED HETERODIMER WITH CD94.
CC -1- SUBCELLULAR LOCATION: TYPE II membrane protein.
CC -1- TISSUE SPECIFICITY: NATURAL KILLER CELLS.
CC -1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
CC
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

DR	EMBL; X54870; CAA36652.1; -	
DR	EMBL; AJ001687; CAA04925.1; -	
DR	EMBL; AJ001688; CAA04925.1; JOINED.	
DR	EMBL; AF001689; CAA04925.1; JOINED.	
DR	PIR; PT0375; PT0375.	
DR	PIR; SI1910; SI1910.	
DR	MIM; 602893; -	
DR	InterPro: IPR001304; lectin_c.	
DR	Pfam: PF00059; lectin_c; 1.	
DR	SMART; SM00034; LECT1; 1.	
DR	PROSITE; PS00615; C_TYPE_LLECTIN_1; FALSE_NEG.	
DR	PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.	
KW	Receptor; Transmembrane; Multigene family; Signal-anchor; Lectin; Glycoprotein.	
FT	DOMAIN 1 51	CYTOPLASMIC (POTENTIAL).
FT	TRANSERM 52 72	SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN) (POTENTIAL).
FT	DOMAIN 73 216	EXTRACELLULAR (POTENTIAL).
FT	DOMAIN 98 213	C-TYPE LECTIN (LONG FORM).
FT	DISULEID 99 110	BY SIMILARITY.
FT	DISULEID 127 211	BY SIMILARITY.
FT	DISULEID 189 203	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBHYD 131 131	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBHYD 163 163	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBHYD 202 202	N-LINKED (GLCNAC. . .) (POTENTIAL).
SO	SEQUENCE 216 AA; 25274 MW; C22FEBD53BD7800E CRC64;	

RP SEQUENCE FROM N.A.  
 RA MEDLINE-98350122; Pubmed-5683661.  
 RX Glienne J., Sobanov Y., Brosstjan C., Steffens C., Nguyen C.,  
 RA Lehnach H., Hofer E., Francis F.,  
 RA "The genomic organization of NKG2C, E, F, and D receptor genes in the  
 RT human natural killer gene complex."  
 RL Immunogenetics 48:163-173(1998).  
 CC -1- FUNCTION: PLAYS A ROLE AS A RECEPTOR FOR THE RECOGNITION OF MHC  
 CC CLASS I HLA-E MOLECULES BY NK CELLS AND SOME CYTOTOXIC T-CELLS.  
 CC -1- SUBUNIT: CAN FORM DISULFIDE-BONDED HETERODIMER WITH CD94.  
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein.  
 CC -1- TISSUE SPECIFICITY: NATURAL KILLER CELLS.  
 CC -1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.  
 CC -----  
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DR	EMBL: L14542; AAI16833.1; .	
DR	EMBL: AJ001685; CAA04923.1; .	
DR	MIM: 602892; .	
DR	InterPro: IPR001304; Lectin_c.	
DR	Pfam: PF00059; Lectin_c; 1.	
DR	SMART: SM00034; CLECT. 1.	
DR	PROSITE: PS00615; C_TYPE_LECTIN_1; FALSE_NEG.	
DR	PROSITE: PS50041; C_TYPE_LECTIN_2; 1.	
KM	Receptor; Transmembrane; Multigene family; Signal-anchor; Lectin;	
KM	Glycoprotein.	
FT	DOMAIN	1 70
FT	TRANSMEM	71 93
FT	DOMAIN	
FT	DOMAIN	94 240
FT	DISULFID	116 230
FT	DISULFID	117 128
FT	DISULFID	207 220
FT	CARBOHYD	100 100
FT	CARBOHYD	149 149
FT	CARBOHYD	179 179
EQ	SEQUENCE	240 AA; 27012 MW; 20691EFB2174D8A6 CRC64;

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0Y      146 GSPLEFRI-----SSNSFYOTGCAIN 167
      |||:::|
Db      171 GSILSPNLTITTEMOKGDCALYASSFKYIENCSTPN 207

RESULT 7
NKG_E_HUMAN
ID      NKG_E_HUMAN      STANDARD;      PRT;      240 AA.
AC      007444;
DT      01-NOV-1997 (Rel. 35, Created)
DT      01-NOV-1997 (Rel. 35, Last sequence update)
DT      01-MAR-2002 (Rel. 41, Last annotation update)
DE      NKG2-E type II integral membrane protein (NKG2-D activating NK
DE      receptor).
GN      KLRG3 OR NKG2E.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=94102823; PubMed=8276468;
RA      Adamkiewicz T.V., McSherry C., Bach F.H., Houchins J.P.;
RT      Natural killer lectin-like receptors have divergent carboxy-termini,
RT      distinct from C-type lectins."
RL      Immunogenetics 39:218-218(1994).
RN      [2]

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Query Match	17.4%	Score 178.5	DB 1	Length 240
Best Local Similarity	28.6%	Pred. No. 6.9e-10		
Matches 46	Conservative 30	Mismatches 70	Indels 15	Gaps 6
QY	24	POKSSSKPSCSCLVAITGLTAVLSTVLYOMILCOGSNST----	CASCPSPDRW 79	
Db	67	PPEKLTAEVLGILIV-----LMAITVLTLYLFLLEGNSSPPTRIQKARPCCHCFEEW 121		
QY	80	MKYGNHCYFSEVEEKDWNSSLFELCARDSHLITVDN-OEMSLQVLEAFWCWIGL-RN 137		
Db	122	ITYSNCCYICKERTWESLIQACASKNSSSLSDNDEEKKFLASILPSS--WIGVFRN 179		
QY	138	NSGWRWEDGSPLNFS--ISSNSFVOTGAIKNKGLOASSC 176		
Db	180	SSHHPWYTINGLAFKHEIKSDHAERNCAMLHVGILISDQC 220		
RESULT	8			
NK13 RAT				
ID	NK13 RAT	STANDARD	PRT	223 AA.
AC	P27471			
DT	01-AUG-1992 (Rel. 23, Created)			
DT	01-AUG-1992 (Rel. 23, Last sequence update)			
DT	01-JUN-1994 (Rel. 29, Last annotation update)			
DE	Natural killer cell surface protein PL-3.2.3 (NKR-PL 3.2.3) (Antigen 3.2.3).			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;			

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OC Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Rattus.
OX NCBI_TaxID-10116;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=90378305; PubMed=2399464;
RA Giordano R., Rudert W.A., Vavassori C., Chambers W.H.,
RA Hissrodt J.C., Trucco M.,
RT "NKR-PI, a signal transduction molecule on natural killer cells.";
RL Science 249:1298-1300(1990).
CC -1- FUNCTION: MEDIATES TRANSMEMBRANE SIGNALING IN NATURAL KILLER
CC (NK) CELLS, AND SO MAY ACT AS A RECEPTOR ABLE TO SELECTIVELY
CC TRIGGER NK CELL ACTIVITY.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: Type II membrane protein.
CC -1- TISSUE SPECIFICITY: NATURAL KILLER CELLS.
CC -1- MISCELLANEOUS: LIGAND BINDING MAY BE CALCIUM DEPENDENT.
CC -1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL, M62891; AAA41710.1; -.
CC PIR, A35917; A35917.
CC InterPro: IPR001304; lectin_c.
CC DR Pfam: PF000059; lectin_c; 1.
CC SMART: SM00034; CLECT; 1.
CC PROSITE: PS00615; C-TYPE_LECTIN_1; FALSE_NEG.
CC DR PROSITE: PS50041; C-TYPE_LECTIN_2; 1.
CC KW Glycoprotein; Antigen; Transmembrane; Signal-anchor; Lectin.
CC FT DOMAIN 1 43 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 44 63 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
CC (POTENTIAL).
CC FT DOMAIN 64 223 EXTRACELLULAR (POTENTIAL).
CC FT FT 93 212 C-TYPE LECTIN (LONG FORM).
CC FT DISULFID 94 105 BY SIMILARITY.
CC FT DISULFID 122 210 BY SIMILARITY.
CC FT CARBOHYD 82 202 BY SIMILARITY.
CC FT CARBOHYD 143 143 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 169 169 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT SEQUENCE 223 AA; 24551 MW; FCD12B212DDF4330 CRC64;

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DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Macrophage asialoglycoprotein-binding protein (M-ASGP-BP) (Macrophage
DE galactose/N-acetylgalactosamine-specific lectin) (MGML).
GN MGML.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Mus.
OX NCBI_TaxID-10090;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=92268032; PubMed=1587794;
RX Sato M., Kawakami K., Osawa T., Toyoshima S.,
RT "Molecular cloning and expression of cDNA encoding a galactose/N-
RT acetylgalactosamine-specific lectin on mouse tumoricidal
RT macrophages.";
RL J. Biochem. 111:331-336(1992).
RN [2]
RN SEQUENCE OF 102-120 AND 137-151.
RP STRAIN=C3H/HEN;
RC MEDLINE=89197865; PubMed=3241002;
RX Oda S., Sato M., Toyoshima S., Osawa T.;
RT "Purification and characterization of a lectin-like molecule specific
RT for galactose/N-acetyl-galactosamine from tumoricidal macrophages.";
RL J. Biochem. 104:600-605(1988).
CC -1- FUNCTION: RECOGNIZES TERMINAL GALACTOSE AND N-ACETYLGALACTOSAMINE
CC UNITS. MAY PARTICIPATE IN THE INTERACTION BETWEEN TUMORICIDAL
CC MACROPHAGES AND TUMOR CELLS.
CC -1- SUBUNIT: HOMO-OLIGOMER.
CC -1- SUBCELLULAR LOCATION: Type II membrane protein.
CC -1- TISSUE SPECIFICITY: IS EXPRESSED ON THE SURFACE OF ACTIVATED
CC MACROPHAGES.
CC -1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL, S36676; AAB22171.1; -.
CC DR HSSP: P06734; IKGE.
CC DR MGD: MGI:96975; MGI.
CC DR InterPro: IPR001304; lectin_c.
CC DR Pfam: PF000059; lectin_c; 1.
CC SMART: SM00034; CLECT; 1.
CC PROSITE: PS00615; C-TYPE_LECTIN_1; 1.
CC DR PROSITE: PS50041; C-TYPE_LECTIN_2; 1.
CC KW Lectin; Glycoprotein; Transmembrane; Calcium; Signal-anchor.
CC FT DOMAIN 1 35 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
CC (POTENTIAL).
CC FT DOMAIN 57 304 EXTRACELLULAR (POTENTIAL).
CC FT FT 172 298 C-TYPE LECTIN (LONG FORM).
CC FT DISULFID 173 184 BY SIMILARITY.
CC FT DISULFID 201 296 BY SIMILARITY.
CC FT DISULFID 274 288 BY SIMILARITY.
CC FT CARBOHYD 74 74 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 166 166 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT SEQUENCE 304 AA; 34596 MW; 3F79CD12C34F5BCC CRC64;

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Query Match 17.28; Score 175.5; DB 1; Length 223;
Best Local Similarity 27.18; Pred. No. 1.2e-09;
Matches 49; Conservative 44; Mismatches 67; Indels 21; Gaps 9;

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Query Match 17.18; Score 174.5; DB 1; Length 304;
Best Local Similarity 27.58; Pred. No. 2.1e-09;
Matches 39; Conservative 27; Mismatches 61; Indels 15; Gaps 5;

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OC Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae: Murinae: Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=90378305; Pubmed=2399464;  
 RA Giorda R., Rudert W.A., Vavasori C., Chambers W.H.,  
 RA Hiserodt J.C., Trucco M.:  
 RT "NKR-PL, a signal transduction molecule on natural killer cells.",  
 RT Science 249:1298-1300(1990).  
 CC -1- FUNCTION: MEDIATES TRANSMEMBRANE SIGNALING IN NATURAL KILLER  
 CC (NK) CELLS. AND SO MAY ACT AS A RECEPTOR ABLE TO SELECTIVELY  
 CC TRIGGER NK CELL ACTIVITY.  
 CC -1- SUBUNIT: HOMODIMER.  
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein.  
 CC -1- TISSUE SPECIFICITY: NATURAL KILLER CELLS.  
 CC -1- MISCELLANEOUS: LIGAND BINDING MAY BE CALCIUM DEPENDENT.  
 CC -1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.  
 CC -----  
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 CC -----  
 CC EMBL: M62891; AAA1710.1; -.  
 DR PIR: A35917; A35917.  
 DR InterPro: IPR001304; lectin\_c.  
 DR Pfam: PF00059; lectin\_c.1.  
 DR SMART: SM00034; CLECT.1.  
 DR PROSITE: PS00615; C-TYPE\_LECTIN\_1; FALSE\_NEG.  
 DR PROSITE: PS00611; C-TYPE\_LECTIN\_2; 1.  
 DR Glycoprotein; Antigen; Transmembrane; Signal-anchor; Lectin.  
 KW DOMAIN 1 43 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 44 63 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)  
 FT 64 63 (POTENTIAL).  
 FT DOMAIN 64 223 EXTRACELLULAR (POTENTIAL).  
 FT DISULFID 93 212 C-TYPE LECTIN (LONG FORM).  
 FT DISULFID 94 105 BY SIMILARITY.  
 FT DISULFID 122 210 BY SIMILARITY.  
 FT DISULFID 189 202 BY SIMILARITY.  
 FT CARBOHYD 82 82 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 143 143 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 169 169 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 169 169 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 223 AA; 24551 MW; FCD12B212DDF4330 CRC64;  
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 Query Match 17.2%; Score 175.5; DB 1; Length 223;  
 Best Local Similarity 27.1%; Pred. No. 1.2e-09;  
 Matches 49; Conservative 44; Mismatches 67; Indels 21; Gaps 9;  
 OY 24 PQQSSSSKPCSCLVATLGL-TAVLLSVLYQ-----WILGGSNSTCASCPS-- 74  
 DB 35 PRSHRLATKSCAGLILVLAVALGMSILVAVYQKRVSECRVLIQ-ENLSKTS-PAKL 92  
 OY 75 -CPDRMKYGNHCYFSVEEKDNSSLEFCLARDSHLLVTTDQEMSLQV--LESAF 130  
 DB 93 KCPKDWLSHRDKCFHVSQTSITWKESLADGGKATLLVQDOBELRRLTRKRISSEF 152  
 OY 131 CWGLR---NSGWRWEDGSPLPFS--RISNSNFOVCGAIKNGKLASSEVPLHGYCK 185  
 DB 153 -WIGLSYTLSDENMKWINGSTNSDVLSTIGDTEKDCASVSQKVLSESCDSNIMVQC 211  
 OY 186 K 186  
 DB 212 K 212  
 RESULT 9  
 MMGL\_MOUSE STANDARD; PRT; 304 AA.  
 AC P49300;

DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE Macrophage asialoglycoprotein-binding protein (M-ASGP-BP) (Macrophage  
 DE galactose/N-acetylgalactosamine-specific lectin) (MMGL).  
 GN MGL.  
 OS Mus musculus (Mouse).  
 OC Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:  
 OC Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae: Murinae: Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C3H/HEN;  
 RA MEDLINE=92268032; Pubmed=1587794;  
 RA Sato M., Kawakami K., Osawa T., Toyoshima S.;  
 RT "Molecular cloning and expression of cDNA encoding a galactose/N-  
 RT acetylgalactosamine-specific lectin on mouse tumoricidal  
 RT macrophages.";  
 RL J. Biochem. 111:331-336(1992).  
 RN [2]  
 RP SEQUENCE OF 102-120 AND 137-151.  
 RC STRAIN=C3H/HEN;  
 RX MEDLINE=89197865; Pubmed=3241002;  
 RA Oda S., Sato M., Toyoshima S., Osawa T.;  
 RT "Purification and characterization of a lectin-like molecule specific  
 RT for galactose/N-acetyl-galactosamine from tumoricidal macrophages.";  
 RL J. Biochem. 104:600-605(1988).  
 CC -1- FUNCTION: RECOGNIZES TERMINAL GALACTOSE AND N-ACETYLGALACTOSAMINE  
 CC UNITS. MAY PARTICIPATE IN THE INTERACTION BETWEEN TUMORICIDAL  
 CC MACROPHAGES AND TUMOR CELLS.  
 CC -1- SUBUNIT: HOMO-OLIGOMER.  
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein.  
 CC -1- TISSUE SPECIFICITY: IS EXPRESSED ON THE SURFACE OF ACTIVATED  
 CC MACROPHAGES.  
 CC -1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL: S36676; AAB22171.1; -.  
 DR HSSP: P06734; IKCE.  
 DR MGD: MGI:96975; MGI.  
 DR InterPro: IPR001304; lectin\_c.  
 DR Pfam: PF00059; lectin\_c.1.  
 DR SMART: SM00034; CLECT.1.  
 DR PROSITE: PS00615; C-TYPE\_LECTIN\_1; 1.  
 DR PROSITE: PS00611; C-TYPE\_LECTIN\_2; 1.  
 KW Lectin; Glycoprotein; Transmembrane; Calcium; Signal-anchor.  
 FT DOMAIN 1 35 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)  
 FT 57 56 (POTENTIAL).  
 FT DOMAIN 57 304 EXTRACELLULAR (POTENTIAL).  
 FT DISULFID 172 298 C-TYPE LECTIN (LONG FORM).  
 FT DISULFID 173 184 BY SIMILARITY.  
 FT DISULFID 201 296 BY SIMILARITY.  
 FT DISULFID 274 288 BY SIMILARITY.  
 FT CARBOHYD 74 74 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 166 166 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 166 166 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 304 AA; 34596 MW; 3F79CD12C34F5BC CRC64;  
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 Query Match 17.1%; Score 174.5; DB 1; Length 304;  
 Best Local Similarity 27.5%; Pred. No. 2.1e-09;  
 Matches 39; Conservative 27; Mismatches 61; Indels 15; Gaps 5;  
 OY 59 ILGGSNSTCASC-CPSPDRMKYGNHCYFSVEEKDNSSLEFCLARDSHLLVTTDQ 117  
 DB 156 LTCQLANLKNNGSEVACPLMTWTEHSGCYWFSESEKSPENDKCYRLNLSLVVNSLE 215

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QY 118 EMLLOYFLSEAFCMIGLRNNSG-WRMEDGSP...NFSRISNSPV-----QFNC 164
DB 216 EQLNLRKLANVWVWIGLTDNGPWRWDGTFDEKFKRMAFLDPDNFGLGSGEDCA 275
QY 165 AINKNG-LQASCEVPLHGVC 185
DB 276 HITGGPMNDVCCORTFRWICE 297

RESULT 10
ID CD69_HUMAN . STANDARD; PRT; 199 AA.
AC 007108:
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Early activation antigen CD69 (Early T-cell activation antigen p60)
DE (GP32/28) (Leu-23) (MLR-3) (EAL) (BL-AC/P26) (Activation inducer
DE molecule) (AIM).
GN CD69.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=93340630; PubMed=8496594;
RA Hamann J., Fiebig H., Strauss M.;
RT Expression cloning of the early activation antigen CD69, a type II
RT integral membrane protein with a C-type lectin domain."
RL J. Immunol. 150:4920-4927(1993).
RN [2]
RP SEQUENCE FROM N.A. AND SEQUENCE OF 96-103; 128-146 AND 189-199.
RC TISSUE=Blood;
RX MEDLINE=93340630; PubMed=8340758;
RA Lopez-Cabrera M., Santis A.G., Fernandez-Ruiz E., Blacher R.,
RA Esch F., Sanchez-Mateos P., Sanchez-Madrid F.;
RT "Molecular cloning, expression, and chromosomal localization of the
RT human earliest lymphocyte activation antigen AIM/CD69, a new member
RT of the C-type animal lectin superfamily of signal-transmitting
RT receptors."
RL J. Exp. Med. 178:537-547(1993).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=93314711; PubMed=8100776;
RA Ziegler S.F., Ramsdell F., Hjertild K.A., Armitage R.J.,
RA Grabstein K.H., Hennen K.B., Farrar T., Fanslow W.C., Shevach E.M.,
RA Alderson M.R.;
RT "Molecular characterization of the early activation antigen CD69: a
RT type II membrane glycoprotein related to a family of natural killer
RT cell activation antigens."
RL Eur. J. Immunol. 23:1643-1648(1993).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=94298875; PubMed=8026529;
RA Santis A., Lopez-Cabrera M., Hamann J., Strauss M., Sanchez-Madrid F.;
RT "Structure of the gene coding for the human early lymphocyte
RT activation antigen CD69: a C-type lectin receptor evolutionarily
RT related with the gene families of natural killer cell-specific
RT receptors."
RL Eur. J. Immunol. 24:1692-1697(1994).
RN [5]
RP FUNCTION: INVOLVED IN LYMPHOCYTE PROLIFERATION AND FUNCTIONS AS A
RN SIGNAL TRANSMITTING RECEPTOR IN LYMPHOCYTES, NATURAL KILLER (NK)
RN CELLS, AND PLATELETS.
RN [6]
RP SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
RN [7]
RP SUBCELLULAR LOCATION: Type II membrane protein.
RN [8]
RP TISSUE SPECIFICITY: EXPRESSED ON THE SURFACE OF ACTIVATED T CELLS,
RN B-CELLS, NATURAL KILLER CELLS, NEUTROPHILS, EOSINOPHILS, EPIDERMAL
RN LANGERHANS CELLS AND PLATELETS.
RN [9]
RP DEVELOPMENTAL STAGE: EARLIEST INDUCIBLE CELL SURFACE GLYCOPROTEIN

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CC ACQUIRED DURING LYMPHOID ACTIVATION.
CC -! INDUCTION: BY ANTIGENS, MITOGENS OR ACTIVATORS OF PKC ON THE
CC SURFACE OF T AND B LYMPHOCYTES. BY INTERACTION OF IL-2 WITH THE
CC P/75 IL-2R ON THE SURFACE OF NK CELLS.
CC -! PM: CONSTITUTIVE SER/THR PHOSPHORYLATION IN BOTH MATURE
CC THYMOCYTES AND ACTIVATED T LYMPHOCYTES.
CC -! DATABASE: NAME=PROW; NOTE=CD guide CD69 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd69.htm".
CC -----
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CC or send an email to license@sdb-sdb.ch).
CC -----
DR EMBL; L07555; AAB46359.1; -
DR EMBL; Z22576; CAA80298.1; -
DR EMBL; Z30426; CAA83017.1; -
DR EMBL; Z30430; CAA83017.1; JOINED.
DR EMBL; Z30427; CAA83017.1; JOINED.
DR EMBL; Z30429; CAA83017.1; JOINED.
DR EMBL; Z30428; CAA83017.1; JOINED.
DR PIR; JH0822; JH0822.
DR MIM; 107273; -
DR InterPro; IPR001304; lectin_c.
DR Pfam; PF00059; lectin_c.1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C-TYPE LECTIN.1; FALSE_NEG.
DR PROSITE; PS50041; C-TYPE LECTIN.2; 1.
KW Antigen; B-cell; Glycoprotein; Transmembrane; Lectin; Signal-anchor;
KW phosphorylation.
FT DOMAIN 1 40 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 1 61 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT DOMAIN 62 199 (POTENTIAL).
FT DOMAIN 67 199 EXTRACELLULAR (POTENTIAL).
FT DISULFID 68 85 C-TYPE LECTIN (LONG FORM).
FT DISULFID 96 194 BY SIMILARITY.
FT DISULFID 173 186 BY SIMILARITY.
FT CARBOHYD 166 166 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 199 AA; 22559 MW; 172E269D2F8BDFB CRC64;

Query Match 17.0%; Score 174; DB 1; Length 199;
Best Local Similarity 22.9%; Pred. No. 1.5e-09;
Matches 40; Conservative 33; Mismatches 76; Indels 26; Gaps 5;

QY 30 SSKPSCSLVATITGLALVAVLSVLLYOMILCOGSNYSCASC-----SC 75
DB 30 STRHGSQVPLCAVMWVFTTILIALISVGOY-----NCPQOYFSPMSDSHVSC 85
QY 76 PDRMKYGNHCYFVSVERKDNNSLEPCARDSHLVITDNGEMSLQVFLSEAFCMIGL 135
DB 86 SEDWVGIOKCFYFTVYKRSWTSAGNACSEHGATLAVIDSEKDMNPLKYAREEHVGL 145
QY 136 RNNSG-WRMEDGSP...NFSRISNSPVQTCGAIINKNGLAQASCEVPLHGVC 186
DB 146 KKEGHPKMSNGKRFNNMFWVTGSDK---CVFLKNFEVSSMECEKKNLYWCNK 196

RESULT 11
ID CLF2_HUMAN . STANDARD; PRT; 149 AA.
AC 092478:
DT 01-MAR-2002 (Rel. 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE C-type lectin superfamily member 2 (Activation-induced C-type lectin).
DE CLECSF2 OR ATCL.
GN Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia:Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97190245; PubMed=9038101;
RA Hamann J., Montgomery K.T., Lau S., Kucheraipati R., van Lier R.A.W.;
RT "AICL, a new activation induced antigen encoded by the human NK gene
complex";
RL Immunogenetics 45:295-300(1997).
CC -1- SUBCELLULAR LOCATION: Type II membrane protein (Probable).
CC -1- TISSUE SPECIFICITY: Expressed preferentially in lymphoid tissues,
CC and in most hematopoietic cell types.
CC -1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
CC -----
CC CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
CC DR EMBL; X96719; CAA65480.1; .
CC DR MIM; 603242; .
CC DR InterPro: IPR001304; lectin_c.
CC DR Pfam: PF00059; lectin_c; 1.
CC DR SMART; SM00034; CLECT; 1.
CC DR PROSITE; PS00615; C-TYPE_LECTIN_1; FALSE_NEG.
CC DR PROSITE; PS50041; C-TYPE_LECTIN_2; 1.
CC KM Glycoprotein; Transmembrane; Lectin; Signal-anchor.
CC FT DOMAIN 1 7 CYTOPLASMIC (POTENTIAL).
CC FT TRANSSEM 8 25 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
CC (POTENTIAL).
CC FT DOMAIN 26 149 EXTRACELLULAR (POTENTIAL).
CC FT DOMAIN 42 145 C-TYPE LECTIN.
CC FT DISULFID 46 63 BY SIMILARITY.
CC FT DISULFID 87 144 BY SIMILARITY.
CC FT DISULFID 123 136 BY SIMILARITY.
CC FT CARBOHYD 57 57 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 62 62 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SO SEQUENCE 149 AA; 17329 MW; 0B4FE2EC7EB36C55 CRC64;

Query Match 16.4%; Score 168; DB 1; Length 149;
Best Local Similarity 31.3%; Pred. No. 4e-09;
Matches 36; Conservative 24; Mismatches 49; Indels 6; Gaps 3;

QY 75 CPDMMKYGKNGICFYFVSEKDMNSSLLECCLADSHLVYITDQMSLLOVFLSEAFQWIG 134
DB 35 CPYDWIGQNCYCYFSYKKEGDWNSKYNCSYTHADLTITDNEENFRLRYKCSSDHWIG 94
QY 135 L---RNNNGMWKEDSPLENFSRISNSNFVOTGCAINKNGLASCEVPLHGVCCK 186
DB 95 LKMAKNRTG-QWVHGA--TFTRKSPGMRSGEGCAYLSDDGAAIARCTYERKWKICRK 146

RESULT 12
LECI_MOUSE
ID LECI_MOUSE STANDARD: PRT: 301 AA.
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Asialoglycoprotein receptor 2 (Hepatic lectin 2) (MHL-2) (ASGP-R)
DE (ASGP-R).
GN ASGR2 OR ASGR-2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBL_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.

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QY	DB	Score	Length	DB 1	DB 2	DB 3	DB 4	DB 5	DB 6	DB 7	DB 8	DB 9	DB 10	DB 11	DB 12	DB 13	DB 14	DB 15	DB 16	DB 17	DB 18	DB 19	DB 20	DB 21	DB 22	DB 23	DB 24	DB 25	DB 26	DB 27	DB 28	DB 29	DB 30	DB 31	DB 32	DB 33	DB 34	DB 35	DB 36	DB 37	DB 38	DB 39	DB 40	DB 41	DB 42	DB 43	DB 44	DB 45	DB 46	DB 47	DB 48	DB 49	DB 50	DB 51	DB 52	DB 53	DB 54	DB 55	DB 56	DB 57	DB 58	DB 59	DB 60	DB 61	DB 62	DB 63	DB 64	DB 65	DB 66	DB 67	DB 68	DB 69	DB 70	DB 71	DB 72	DB 73	DB 74	DB 75	DB 76	DB 77	DB 78	DB 79	DB 80	DB 81	DB 82	DB 83	DB 84	DB 85	DB 86	DB 87	DB 88	DB 89	DB 90	DB 91	DB 92	DB 93	DB 94	DB 95	DB 96	DB 97	DB 98	DB 99	DB 100	DB 101	DB 102	DB 103	DB 104	DB 105	DB 106	DB 107	DB 108	DB 109	DB 110	DB 111	DB 112	DB 113	DB 114	DB 115	DB 116	DB 117	DB 118	DB 119	DB 120	DB 121	DB 122	DB 123	DB 124	DB 125	DB 126	DB 127	DB 128	DB 129	DB 130	DB 131	DB 132	DB 133	DB 134	DB 135	DB 136	DB 137	DB 138	DB 139	DB 140	DB 141	DB 142	DB 143	DB 144	DB 145	DB 146	DB 147	DB 148	DB 149	DB 150	DB 151	DB 152	DB 153	DB 154	DB 155	DB 156	DB 157	DB 158	DB 159	DB 160	DB 161	DB 162	DB 163	DB 164	DB 165	DB 166	DB 167	DB 168	DB 169	DB 170	DB 171	DB 172	DB 173	DB 174	DB 175	DB 176	DB 177	DB 178	DB 179	DB 180	DB 181	DB 182	DB 183	DB 184	DB 185	DB 186	DB 187	DB 188	DB 189	DB 190	DB 191	DB 192	DB 193	DB 194	DB 195	DB 196	DB 197	DB 198	DB 199	DB 200	DB 201	DB 202	DB 203	DB 204	DB 205	DB 206	DB 207	DB 208	DB 209	DB 210	DB 211	DB 212	DB 213	DB 214	DB 215	DB 216	DB 217	DB 218	DB 219	DB 220	DB 221	DB 222	DB 223	DB 224	DB 225	DB 226	DB 227	DB 228	DB 229	DB 230	DB 231	DB 232	DB 233	DB 234	DB 235	DB 236	DB 237	DB 238	DB 239	DB 240	DB 241	DB 242	DB 243	DB 244	DB 245	DB 246	DB 247	DB 248	DB 249	DB 250	DB 251	DB 252	DB 253	DB 254	DB 255	DB 256	DB 257	DB 258	DB 259	DB 260	DB 261	DB 262	DB 263	DB 264	DB 265	DB 266	DB 267	DB 268	DB 269	DB 270	DB 271	DB 272	DB 273	DB 274	DB 275	DB 276	DB 277	DB 278	DB 279	DB 280	DB 281	DB 282	DB 283	DB 284	DB 285	DB 286	DB 287	DB 288	DB 289	DB 290	DB 291	DB 292	DB 293	DB 294	DB 295	DB 296	DB 297	DB 298	DB 299	DB 300	DB 301	DB 302	DB 303	DB 304	DB 305	DB 306	DB 307	DB 308	DB 309	DB 310	DB 311	DB 312	DB 313	DB 314	DB 315	DB 316	DB 317	DB 318	DB 319	DB 320	DB 321	DB 322	DB 323	DB 324	DB 325	DB 326	DB 327	DB 328	DB 329	DB 330	DB 331	DB 332	DB 333	DB 334	DB 335	DB 336	DB 337	DB 338	DB 339	DB 340	DB 341	DB 342	DB 343	DB 344	DB 345	DB 346	DB 347	DB 348	DB 349	DB 350	DB 351	DB 352	DB 353	DB 354	DB 355	DB 356	DB 357	DB 358	DB 359	DB 360	DB 361	DB 362	DB 363	DB 364	DB 365	DB 366	DB 367	DB 368	DB 369	DB 370	DB 371	DB 372	DB 373	DB 374	DB 375	DB 376	DB 377	DB 378	DB 379	DB 380	DB 381	DB 382	DB 383	DB 384	DB 385	DB 386	DB 387	DB 388	DB 389	DB 390	DB 391	DB 392	DB 393	DB 394	DB 395	DB 396	DB 397	DB 398	DB 399	DB 400	DB 401	DB 402	DB 403	DB 404	DB 405	DB 406	DB 407	DB 408	DB 409	DB 410	DB 411	DB 412	DB 413	DB 414	DB 415	DB 416	DB 417
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[illegible]

DR	MGP; MG1:101907; K1ral.	
DR	InterPro; IPR001304; lectin_c.	
DR	Pfam; PF00059; lectin_c; 1.	
DR	SMART; SM00034; CLECT; 1.	
DR	PROSITE; PS00615; C-TYPE LECTIN.1; FALSE_NEG.	
DR	PROSITE; PSS00041; C-TYPE LECTIN.2; 1.	
KW	T-cell; glycoprotein; Antigen; Transmembrane; Cell adhesion;	
KW	Signal_anchor; Lectin; Receptor; Multigene family.	
FT	DOMAIN	1
FT	TRANSMEM	45
FT		66
FT		44
FT	DOMAIN	67
FT	DOMAIN	138
FT	DISULFID	167
FT	DISULFID	232
FT	DISULFID	245
FT	SITE	137
FT	CARBOHYD	86
FT	CARBOHYD	86
FT	CARBOHYD	123
FT	CARBOHYD	103
FT	CONFLICT	76
FT	CONFLICT	106
FT	CONFLICT	166
FT	CONFLICT	166
FT	CONFLICT	223
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SO	SEQUENCE	262 AA; 30498 MW; 3C3328D5265F1B5E CRC64;

Query Match	15.88;	Score 162;	DB 1;	Length 262;
Best Local Similarity	21.7%;	Pred. No. 2.7e-08;		
Matches 55; Conservative	32;	Mismatches 92;	Indels 74;	Gaps 9;

[illegible]

Search completed: September 9, 2002, 15:03:58  
Job time: 232 sec

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## OM protein - protein search, using sw model

Run on: September 9, 2002, 14:41:21 ; Search time 13.1 Seconds

(without alignments)  
352,400 Million cell updates/sec

Title: US-09-811-367b-1

Perfect score: 1023

Sequence: 1 MDSVYISMELPFAAQON.....GLQASCEPLHGCKKRVRL 189

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_AA.\*  
1: /cgn2\_6/ptodata/2/1aa/5A.COMB.pep.\*  
2: /cgn2\_6/ptodata/2/1aa/5B.COMB.pep.\*  
3: /cgn2\_6/ptodata/2/1aa/6A.COMB.pep.\*  
4: /cgn2\_6/ptodata/2/1aa/6B.COMB.pep.\*  
5: /cgn2\_6/ptodata/2/1aa/PCRTUS.COMB.pep.\*  
6: /cgn2\_6/ptodata/2/1aa/Backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	525.5	51.4	188	3	US-08-722-126A-5
2	525.5	51.4	188	3	PCT-US95-04258-5
3	370.5	36.2	114	3	US-08-722-126A-6
4	370.5	36.2	114	5	PCT-US95-04258-6
5	201	19.6	225	2	US-08-738-462-2
6	201	19.6	225	5	PCT-US94-07587-2
7	196.5	19.2	179	1	US-08-690-095-9
8	196.5	19.2	179	2	US-08-650-578-2
9	196.5	19.2	179	2	US-08-688-342-3
10	196.5	19.2	179	2	US-09-113-788-3
11	196.5	19.2	179	3	US-09-113-789-9
12	196.5	19.2	199	5	PCT-US93-10418-4
13	193	18.9	270	2	US-09-055-095-4
14	193	18.9	270	2	US-08-809-494A-2
15	193	18.9	270	4	US-09-352-302-2
16	193	18.9	273	4	US-08-809-494A-4
17	193	18.9	273	4	US-09-352-302-4
18	190	18.6	233	1	US-08-690-095-8
19	190	18.6	233	3	US-09-113-789-8
20	190	18.6	233	4	US-08-543-246B-2
21	190	18.6	233	4	US-08-543-246B-21
22	185.5	18.1	215	4	US-09-111-470-4
23	184	18.0	215	3	US-08-690-095-7
24	184	18.0	215	3	US-09-113-789-7
25	184	18.0	215	4	US-08-543-246B-16
26	184	18.0	215	4	US-08-543-246B-22
27	182	17.8	231	1	US-08-690-095-6

28	182	17.8	231	3	US-09-113-789-6	Sequence 6, Appl
29	182	17.8	231	4	US-08-543-246B-6	Sequence 6, Appl
30	182	17.8	231	4	US-08-543-246B-23	Sequence 23, Appl
31	181	17.7	273	2	US-09-055-095-3	Sequence 3, Appl
32	181	17.7	273	2	US-08-809-494A-6	Sequence 6, Appl
33	181	17.7	273	4	US-09-352-302-6	Sequence 6, Appl
34	180	17.6	216	4	US-08-543-246B-9	Sequence 9, Appl
35	180	17.6	216	4	US-08-543-246B-24	Sequence 24, Appl
36	179.5	17.5	273	4	US-09-111-470-10	Sequence 10, Appl
37	179.5	17.5	292	2	US-08-688-342-4	Sequence 4, Appl
38	179.5	17.5	292	2	US-09-113-788-4	Sequence 4, Appl
39	175.5	17.2	168	3	US-08-772-440-17	Sequence 17, Appl
40	175.5	17.2	201	2	US-08-688-342-1	Sequence 1, Appl
41	175.5	17.2	201	2	US-09-113-788-1	Sequence 1, Appl
42	174	17.0	199	5	PCT-US93-10418-2	Sequence 2, Appl
43	173	16.9	175	3	US-08-772-440-15	Sequence 15, Appl
44	173	16.9	209	3	US-08-772-440-4	Sequence 4, Appl
45	172	16.8	134	3	US-08-772-440-16	Sequence 16, Appl

## ALIGNMENTS

RESULT 1  
US-08-722-126A-5  
; Sequence 5, Application US/08722126A  
; Patent No. 6034227  
; GENERAL INFORMATION:  
; APPLICANT: PECHT, Israel  
; APPLICANT: GUTHMANN, Marcelo D.  
; APPLICANT: TAL, Michael  
; TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL  
; TITLE OF INVENTION: FUNCTION-ASSOCIATED ANTIGEN (MAFA).  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.  
; STREET: 419 Seventh Street N.W., Ste. 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: UNITED STATES OF AMERICA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/722,126A  
; FILING DATE: 08-OCT-1996  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/04258  
; FILING DATE: 06-APR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: IL 109257  
; FILING DATE: 08-APR-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BROWDY, Roger L.  
; REGISTRATION NUMBER: 25,618  
; REFERENCE/DOCKET NUMBER: PECHT-1A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 628-5197  
; TELEFAX: (202) 737-3528  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 188 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-722-126A-5

Query Match 51.4%; Score 525.5; DB 3; Length 188;



RESULT 4  
PCT-US95-04258-6  
Sequence 6, Application PC/TUS9504258  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL  
FUNCTION-ASSOCIATED ANTIGEN (MAFA)  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419, Seventh Street, N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/04258  
FILING DATE: 06-APR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: IL 109257  
FILING DATE: 08-APR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: BROWDY, Roger L.  
REGISTRATION NUMBER: 25,618  
REFERENCE/DOCKET NUMBER: PECHT-1 PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
TELEX: 248633  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 114 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US95-04258-6

Query Match 36.2%; Score 370.5; DB 5; Length 114;  
Best Local Similarity 58.4%; Pred. No. 1.5e-32;  
Matches 66; Conservative 18; Mismatches 28; Indels 1; Gaps 1;

QY 75 CPBRMKNYGHCHYFSEVEMDNMSLEFCLARDSHLLVITPDNOMSLLOVFLSEAFWIG 134  
DB 1 CPNLMWNSHCHYFSEVEMDNMSLEFCLARDSHLLVITPDNOMSLLOVFLSEAFWIG 60

QY 135 LRNSGWRMGDSPLNFSRISNSFVOTCGAINKNGLOASSCEVPLHGCVCKV 187  
DB 61 LRDDGWRMGDSPLNFSRISNSFVOTCGAINKNGLOASSCEVPLHGCVCKV 112

RESULT 5  
US-08-738-462-2  
Sequence 2, Application US/08738462  
Patent No. 5965401  
GENERAL INFORMATION:  
APPLICANT: Chang, Chiwen  
APPLICANT: Lanier, Lewis L.  
APPLICANT: Phillips Jr., Joseph H.  
TITLE OF INVENTION: Purified Mammalian NK Antigen and  
RELATED REAGENTS  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DNA Research Institute  
STREET: 901 California Avenue  
CITY: Palo Alto

STATE: California  
COUNTRY: USA  
ZIP: 94304-1104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/738,462  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/093,435  
FILING DATE: 16-JUL-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Ching, Edwin P.  
REGISTRATION NUMBER: 34,090  
REFERENCE/DOCKET NUMBER: DX0397  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-852-9196  
TELEFAX: 415-496-1200  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 225 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-738-462-2

Query Match 19.6%; Score 201; DB 2; Length 225;  
Best Local Similarity 26.0%; Pred. No. 6.2e-14;  
Matches 58; Conservative 36; Mismatches 81; Indels 48; Gaps 8;

QY 1 MTDVITYSMLEPRTAONQNDYGPQKSSSKP-----SCSCVAITIG 44  
DB 1 MDQAIYAEMLPRT-----DSGPSSPSPLRDVCGSPWHPALKISCGITLV- 53

QY 45 LITAVILSVLLYOWILCOGSNYSFCA-----SCSPCDRMKYGNCYYS 90  
DB 54 VYTGISVYV-----SLIKSSIEKCSVDIQSRNKTTERPGLINPIYQOLRECLIFS 109

QY 91 VEKDNMSLEFCLARDSHLLVITPDNOMSLLOVFLSE--AFCWIGLR--NNSGWRMGD 145  
DB 110 HTVNMWNSLADCSFKESLLIRKDELHTQNLIRKAILFWIGLNFSLSEKMWKWIN 169

QY 146 GSPLNFS--RISNSFVOTCGAINKNGLOASSCEVPLHGCVCK 186  
DB 170 GSPLNNDLEIRGDAKENSICISISQTSYSEYCSYETIRWICOK 212

RESULT 6  
PCT-US94-07587-2  
Sequence 2, Application PC/TUS9407587  
GENERAL INFORMATION:  
APPLICANT: Schering Corp.  
TITLE OF INVENTION: PURIFIED MAMMALIAN NK ANTIGENS AND  
RELATED REAGENTS  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Schering Corp.  
STREET: One Giralda Farms  
CITY: Madison  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07940  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Macintosh 7.1  
SOFTWARE: Microsoft Word 5.1a  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/07587  
 FILING DATE:  
 CLASSIFICATION:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Lunn, Paul G.  
 REGISTRATION NUMBER: 32,743  
 REFERENCE/DOCKET NUMBER: DX0397K  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 201-822-7255  
 TELEFAX: 201-822-7039  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 225 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 PCT-US94-07587-2

Query Match 19.6%; Score 201; DB 5; Length 225;  
 Best local similarity 26.0%; Pred. No. 6.2e-14;  
 Matches 58; Conservative 36; Mismatches 81; Indels 48; Gaps 8;

QY 1 MTSVITSMLEPRTAQAQNDYGPQKSSSKP-----SCSCVAITLG 44  
 DB 1 MDQATIAELNLP-----DSGPSSPSLPDVCQSPWHOFALKLSGAILLV- 53  
 QY 45 LTPAVLSVLLQWILCOGSMYSTCA-----SCSPCDPMKMYGNHCYFS 90  
 DB 54 VVTGLSVST-----SLQKSIKCSVDIQSRNKTTPGILNPIYQGLRECLLF 109  
 QY 91 VEKDMNSLEFCLARDSHLLVTDNOMSLQVFLSE--APCWIGLR---NNSGWRMD 145  
 DB 110 HTVPMNNNSLDLCSTKESLLIRDKDLHTQNLIRKALLFWIGLNFSLSEKMKWIN 169  
 QY 146 GSPNFS--RISSNSFVOTGAINKNGLOASSCEVPLHGCKK 186  
 DB 170 GSPNFSNDELTRGDKNKSCISOTSYSYCESTEIRWICK 212

## RESULT 7

US-08-690-095-9

Sequence 9, Application US/08690095  
 Patent No. 5792648  
 GENERAL INFORMATION:  
 APPLICANT: Hillman, Jennifer L.  
 APPLICANT: Au-Young, Janice  
 APPLICANT: Goli, Surya K.  
 TITLE OF INVENTION: NOVEL HUMAN MACROPHAGE ANTIGEN  
 NUMBER OF SEQUENCES: 9  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Incyte Pharmaceuticals, Inc.  
 STREET: 3174 Porter Drive  
 CITY: Palo Alto  
 STATE: CA  
 COUNTRY: U.S.  
 ZIP: 94304  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FASTSEQ Version 1.5  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/690,095  
 FILING DATE: Filed herewith  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Billings, Lucy J.  
 REGISTRATION NUMBER: 36,749  
 REFERENCE/DOCKET NUMBER: PF-0110 US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415-855-0555  
 TELEFAX: 415-845-4166  
 INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 179 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 IMMEDIATE SOURCE:  
 LIBRARY: GenBank  
 CLONE: 1098617  
 US-08-690-095-9

Query Match 19.2%; Score 196.5; DB 1; Length 179;  
 Best local similarity 32.7%; Pred. No. 1.4e-13;  
 Matches 53; Conservative 25; Mismatches 69; Indels 15; Gaps 7;

QY 35 CSCLVATLGLTAVLSVLLQWILCOGSM--YSTCASCSPCDPMKMYGNHCYFS 92  
 DB 20 CLSLMA-FLGILKNSFKLSIEPAFTPGPIELQKSDPCSCQKRWGRCNYFISSE 78  
 QY 93 EKDMNSLEFCLARDSHLLVTDNOMSLQVFLSEAPCWIGL---RNSGWRMDGSP 149  
 DB 79 QTWNSRHLCASOKSSLLQONTDELDFMS--SSQFTWIGLSTSEHTAWMGSL 136  
 QY 150 NPSRISSNSF---VOTGAINKNG--LOASSCEVPLHGCKK 186  
 DB 137 --SQTLPSPFETFNKNCIAYNPNGNALDESCEDKNRYICKQ 176

## RESULT 8

US-08-650-578-2

Sequence 2, Application US/08650578  
 Patent No. 5811284  
 GENERAL INFORMATION:  
 APPLICANT: Chang, Chiwen  
 APPLICANT: Aramburu Beltran, Jose  
 APPLICANT: Lopez-Botet, Miguel  
 APPLICANT: Phillips Jr., Joseph H.  
 APPLICANT: Lanier, Lewis L.  
 TITLE OF INVENTION: Purified Mammalian NK Antigens and  
 TITLE OF INVENTION: Related Reagents  
 NUMBER OF SEQUENCES: 2  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: DNAX Research Institute  
 STREET: 901 California Avenue  
 CITY: Palo Alto  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94304-1104  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/650,578  
 FILING DATE:  
 CLASSIFICATION: 514  
 PRIOR APPLICATION NUMBER:  
 APPLICATION NUMBER: US 08/175,339  
 FILING DATE: 29-DEC-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Ching, Edwin P.  
 REGISTRATION NUMBER: 34,090  
 REFERENCE/DOCKET NUMBER: DX0391  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415-852-9196  
 TELEFAX: 415-496-1200  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 179 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear





COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/055,095  
FILING DATE: Filed Herewith  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0500 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-855-0555  
TELEFAX: 650-845-4166  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 270 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: GenBank  
CLONE: 1902982  
US-09-055-095-4

Query Match 18.9%; Score 193; DB 2; Length 270;  
Best Local Similarity 30.6%; Pred. No. 5.7e-13;  
Matches 44; Conservative 25; Mismatches 53; Indels 22; Gaps 5;

QY 57 OMILCGSNVSTCASCPDPRMKYGNHCYFSEVEKDMNSLFCIARDSHLVIYTDN 116  
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |  
DB 127 QEVLEKANNYS-----GPCPDMLHHEENCYQFSSGFNWEKQENCLSDAHLKINST 181  
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |  
QY 117 QEMSLQVFLSEAF--CWIGL---RNSGMRWEDGSPLN-----FSRISSNSFVQT 162  
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |  
DB 182 DLEFIQOMIAHSSFPFMWGLSMRKPNYSWLMEDGTPLPPLHFRIGAVSRMYPG---T 238  
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |  
QY 163 CGAINKNGIQAASCEVPLHGVCKR 186  
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |  
DB 239 CAVIORGTVAENCILITAFSICOK 262  
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

RESULT 14  
US-08-809-494A-2  
Sequence 2, Application US/08809494A  
Patent No. 5962260  
GENERAL INFORMATION:  
APPLICANT: Sawamura, Tatsuya  
APPLICANT: Masaki, Tomoo  
TITLE OF INVENTION: Modified low-Density Lipoprotein  
TITLE OF INVENTION: Receptor  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McAlay Fisher Nissen Goldberg & Kiel  
STREET: 261 Madison Avenue  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10016-2391  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/809,494A  
FILING DATE: 24-MAR-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-321705  
FILING DATE: 30-NOV-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 7-214206  
FILING DATE: 31-JUL-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Goldberg, Jules E  
REGISTRATION NUMBER: 24408  
REFERENCE/DOCKET NUMBER: JG-YT-4363PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212 986-4090  
TELEFAX: 212 818-9479  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 270 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-809-494A-2

Query Match 18.9%; Score 193; DB 2; Length 270;  
Best Local Similarity 30.6%; Pred. No. 5.7e-13;  
Matches 44; Conservative 25; Mismatches 53; Indels 22; Gaps 5;

QY 57 OMILCGSNVSTCASCPDPRMKYGNHCYFSEVEKDMNSLFCIARDSHLVIYTDN 116  
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |  
DB 127 QEVLEKANNYS-----GPCPDMLHHEENCYQFSSGFNWEKQENCLSDAHLKINST 181  
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |  
QY 117 QEMSLQVFLSEAF--CWIGL---RNSGMRWEDGSPLN-----FSRISSNSFVQT 162  
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |  
DB 182 DLEFIQOMIAHSSFPFMWGLSMRKPNYSWLMEDGTPLPPLHFRIGAVSRMYPG---T 238  
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |  
QY 163 CGAINKNGIQAASCEVPLHGVCKR 186  
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |  
DB 239 CAVIORGTVAENCILITAFSICOK 262  
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

RESULT 15  
US-09-352-302-2  
Sequence 2, Application US/09352302  
Patent No. 6197937  
GENERAL INFORMATION:  
APPLICANT: Sawamura, Tatsuya  
APPLICANT: Masaki, Tomoo  
TITLE OF INVENTION: Modified low-Density Lipoprotein  
TITLE OF INVENTION: Receptor  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McAlay Fisher Nissen Goldberg & Kiel  
STREET: 261 Madison Avenue  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10016-2391  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/352,302  
FILING DATE: 12-JUL-1999  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-321705  
FILING DATE: 30-NOV-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 7-214206

FILING DATE: 31-JUL-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Goldberg, Jules E  
 REGISTRATION NUMBER: 24408  
 REFERENCE/DOCKET NUMBER: JG-YY-4363PCT/D  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 212 986-4090  
 TELEFAX: 212 818-9479  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 270 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-09-352-302-2

Query Match 18.9%; Score 193; DB 4; Length 270;  
 Best Local Similarity 30.6%; Pred. No. 5.7e-13;  
 Matches 44; Conservative 25; Mismatches 53; Indels 22; Gaps 5;

QY	57	QWILQGSNYSSTCASCPCPDPMKYNHGYFVSEKDMNSLSEFCLARDSHLVTDN	116
DB	127	QEVLEKAAVNS-----GPCPDMLWHEHCYQFSSGPFNWEKSEQENCLSIDAHLTKINST	181
QY	117	QEMSLQVFLSEAF--CWIGL---RNSGWRNEDGSPLN-----FSRISSNSFVOT	162
DB	182	DELEPIQQWIAHSSPFPMWGLSMRKPNYSWLMWEDGTPLPHLFRIQGAVERMYPG--T	238
QY	163	CGAINKNGLOASSCEVPLHGVCCK	186
DB	239	CAVIOGTIVFAENCILITAFSTICOK	262

Search completed: September 9, 2002, 15:00:04  
 Job time: 1123 sec





PD		XX	11-OCT-2001.
PP		XX	
PR		XX	30-MAR-2001; 2001WO-US08631.
PS		XX	
PT		XX	31-MAR-2000; 2000US-0540217.
QA		XX	23-AUG-2000; 2000US-0649167.
QB		XX	(HYSE-) HYSEQ INC.
QC		XX	
QD		XX	Dermanac RT, Liu C, Tang YT;
QE		XX	
RF		DR	WPI: 2001-639333/73.
RH		DR	N-P.SDE: AAS69638.
RI		XX	
RJ		XX	New isolated polynucleotide and encoded polypeptides, useful in
RK		PT	diagnostics, forensics, gene mapping, identification of mutations
RL		PT	responsible for genetic disorders or other traits and to assess
RM		PT	biodiversity -
RP		XX	
RS		XX	Claim 20; SEQ ID No 35810; 103bp; English.
RT		CC	The invention relates to isolated polynucleotide (I) and
RU		CC	polypeptide (II) sequences. (I) is useful as hybridisation probes,
RV		CC	polymerase chain reaction (PCR) primers, oligomers, and for chromosome
RW		CC	and gene mapping, and in recombinant production of (II). The
RX		CC	polynucleotides are also used in diagnostics as expressed sequence tags
RY		CC	for identifying expressed genes. (I) is useful in gene therapy techniques
RZ		CC	to restore normal activity of (II) or to treat disease states involving
S0		CC	(II). (II) is useful for generating antibodies against it, detecting or
S1		CC	quantitating a polypeptide in tissue, as molecular weight markers and as
S2		CC	a food supplement. (II) and its binding partners are useful in medical
S3		CC	imaging of sites expressing (II). (I) and (II) are useful for treating
S4		CC	disorders involving aberrant protein expression or biological activity.
S5		CC	The polypeptide and polynucleotide sequences have applications in
S6		CC	diagnostics, forensics, gene mapping, identification of mutations
S7		CC	responsible for genetic disorders or other traits to assess biodiversity
S8		CC	and to produce other types of data and products dependent on DNA and
S9		CC	amino acid sequences. ABG00010-ABG30377 represent novel human
SA		CC	diagnostic amino acid sequences of the invention.
SB		CC	Note: The sequence data for this patent did not appear in the printed
SC		CC	specification, but was obtained in electronic format directly from WIPO
SD		XX	at ftp.wipo.int/pub/published_pct_sequences.
SE		XX	
SF		SQ	Sequence 843 AA:
SG			
SH			
SI			
SJ			
SK			
SL			
SM			
SN			
SO			
SP			
SQ			
SR			
SS			
ST			
SU			
SV			
SW			
SX			
SY			
SZ			
T0			
T1			
T2			
T3			
T4			
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TA			
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TC			
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UD			
UE			
UF			
UG			
UH			
UI			
UI			
UJ			
UK			
UL			
UM			
UN			
UN			
UU			
UV			
UV			
UX			
UY			
UZ			
V0			
V1			
V2			
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V7			
V8			
V9			
VA			
VB			
VC			
VD			
VE			
VF			
VG			
VH			
VI			
VJ			
VK			
VL			
VM			
VN			
VO			
VP			
VP			

XX		Mouse; pharmaceutical composition; mast cell function associated antigen;
KW		MAFA; natural killer cell; NK; tumour; therapy; cytotoxic T-cell; CTL;
KW		Immunosuppressive; cytostatic.
XX		
OS	Mus sp.	
XX		
FH	Key	Location/Qualifiers
FT	Domain	64..188 /note= "Extracellular domain"
PX		
PN	MO200170805-A2.	
XX		
PD	27-SEP-2001.	
XX		
PF	16-MAR-2001; 2001WO-US08596.	
XX		
PR	17-MAR-2000; 2000US-190716P.	
XX		
PA	(GEM1-) GEMINI SCI INC.	
PI	Takahashi N, Miyayama T;	
XX		
XX	WPI: 2001-611482/70.	
DR	N-PDB: AAD18735.	
PT		
XX		
XX		
PS	Example 1, Page 19; 49pp; English.	
XX		
CC	The present invention relates to a pharmaceutical composition comprising	
CC	an agent which specifically binds to a mast cell function associated	
CC	antigen (MAFA) ligand on a target cell, and prevents or inhibits natural	
CC	killer (NK)- or T-cell-expressed cell surface MAFA from binding to MAFA	
CC	ligand and a pharmaceutically acceptable excipient. The invention is	
CC	useful for inhibiting an NK- or a T-cell-expressed cell surface MAFA	
CC	binding to a ligand on a target cell, by contacting the pharmaceutical	
CC	composition in vitro, ex vivo or in vivo by administering the composition	
CC	to the subject, to NK or T-cell or the target cell e.g. tumour cell, in	
CC	an amount sufficient to inhibit cell surface MAFA binding to the ligand	
CC	on the target cell. The agent or the composition is useful for treating a	
CC	tumour by stimulating the cytotoxic activity of an NK cell or a cytotoxic	
CC	T-cell (CTL), where the tumour comprises an NK cell- or CTL-susceptible	
CC	tumour cell. The invention is also useful for inhibiting an activity of	
CC	NK cell or a T-cell. The present sequence is mouse MAFA protein.	
XX		
SQ	Sequence 188 AA:	
	Query Match 53.6%; Score 548.5; DB 22; Length 188;	
	Best Local Similarity 55.6%; Pred. No. 4.8e-49;	
	Matches 104; Conservative 26; Mismatches 56; Indels 1; Gaps 1	
OY	1 MTDVSYMELEPTAQANDYGPOOKSSSKSCSCLVAITLGLTAVLVLLYLWIL 60	
Db	1 madsisyltellepeapgydqdesrwkikavlhnphlsrfamwalgiltvlmslmwygrll 60	
OY	61 COGSNTSTCASCPSPDWMKMTGNHCYTFSEVERKNSSLEFLCARDSHLVLTINQEMS 120	
Db	61 ccgsdstcscshpscpilwtirngshcyfismekbkwnsslkfcadqyslhlffpdnqyxp 120	
OY	121 LLQVLTSAFCMIGLRNNSGMREHGSPINFESRISNSFVFQCGAILINKGLQASSCEVPL 180	
Db	121 lfgeylgdqdfwlgitrlnidgwzwegspalsl-riltlnslidqcgahnrngldqasceval 179	
OY	181 HGVCCKV 187	
Db	180 qwlckkv 186	
RESULT	5	

AAR7033	ID AAR7033 standard; Protein; 188 AA.
XX AC AAR7033;	
XX DT 01-FEB-1996 (first entry)	
XX XX Mammalian mast cell function-associated antigen (MAFA).	
DE KW Mast cell function-associated antigen; MAFA; soluble; ligand.	
KW Identification; screening; Inflammation; inflammatory; allergy.	
XX allergic; prevention.	
OS Rattus rattus.	
XX PN W09527734-AI..	
XX PD 19-OCT-1995.	
PX PF 06-APR-1995; 95WO-US04258.	
PR PR 08-APR-1994; 94IL-0109257.	
PA (RYCU/) RYCUS A.	
XN (YEDA ) YEDA RES & DEV CO LTD.	
PI Gutmann MD, Pecht I, Tal M;	
DR WP1: 1995-366356/47.	
N-PSTD; NMT01471.	
PT Novel DNA encoding a mast cell function-associated antigen (MAFA) -	
PS useful for screening for ligands of MAFA which are useful for	
CC prevention of inflammatory and allergic reactions	
XX Claim 12; Page 37; 54pp: English.	
CC A soluble form of mast cell function-associated antigen (MAFA) can	
CC be produced by recombinant techniques for use in the ligand-	
CC screening assay. The ligands that are identified may be used alone	
CC or in combination with the MAFA to prevent inflammatory and allergic	
CC reactions.	
SQ Sequence 188 AA:	
OY Query Match 51.4%; Score 525.5; DB 16; Length 188; Best Local Similarity 53.5%; Pred. No. 1,2e-46;	
DMatches 100; Conservative 29; Mismatches 57; Indels 1; Gaps 1	
OY 1 MTDSIVYSMLLPATYAONDYGPOKSSSKPSCSLVARTLGLTAVLSVLTYOWTL 60   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   Db 1 madmsnystcltelpaprvqddsrwvfkavlhpcvsylmvaalglitvlmlsalilyqrfl 60	
OY 61 CGGSNYSTCASCPSPDDMMKKYGNKYCYFSVEEKDMNSLEFLCLARDSHLTVTTOEWS 120     :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   Db 61 ccgshygfncsgcstrpnltwmrnghocyyfsmekrdwnslkicadkgshlltfpdnqvyn 120	
OY 121 LLQVFLSAFCFWIGIRLNNSGWRMEDGPSLFNRISSNSEFYTGCALINKNGLOASSCEVP 180    :    :    :    :    :    :    :    :    :    :    :    :    :    :    :    :    Db 121 lfgeyvgsdfwyigrlrididgwvrwedgpalsls-ilnsnvvgkcgtlhcrcglhasseceval 179	
OY 181 HGVCCKV 187   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   Db 180 qwlcekV 186	
RESULT 6	
AAW88277 ID AAW88277 standard; Protein; 188 AA. AC AAW88277;	

DF		29-MAR-1999	(first entry)	
XX				
DE	Rat mast cell function-associated antigen (MAFA).			
KX	Mast cell function-associated antigen; MAFA; splice variant; rat;			
KW	inflammation; allergy; asthma; rheumatoid arthritis; tumour;			
KV	therapy.			
XX				
OS	Rattus sp.			
XX				
FH	Key	Location/Qualifiers		
FT	Modified-site	82..84		
FT		/note= "Asn is N-glycosylated"		
FT	Modified-site	97..99		
FT		/note= "Asn is N-glycosylated"		
FN				
PN	MO9654209-A2.			
XX				
PD	03-DEC-1998.			
XX				
PF	29-MAY-1998;	98WO-GB01572.		
XX				
PR	31-MAY-1997;	97GB-0011148.		
XX				
PA	(PEPT-) PEPTIDE THERAPEUTICS LTD.			
XX				
PI	Hewitt, EL, Lamers MBAC, Lamont A, Williams DH;			
XX				
DR	WPI: 1999-059806/05.			
DR	N-PsDB: AAV84222.			
XX				
PT	New polypeptide having a sequence corresponding to human mast cell			
PT	function-associated antigen - useful in forming and manufacturing			
PT	pharmaceutical compositions in the treatment of inflammatory and			
PT	allergic diseases, and tumour growth			
XX				
PS	Disclosure: Fig 4; 44pp: English.			
XX				
CC	This is the amino acid sequence of rat mast cell function-associated			
CC	antigen (MAFA), a type II membrane glycoprotein found on mast cells			
CC	and basophils. The invention relates to cloning of the human MAFA			
CC	molecule (see AAM88265) and to the discovery of splice variants (see			
CC	AAM88266-67) of human MAFA that are not found in rat. Polypeptides			
CC	and synthetic peptides (see AAM88258-64) based on human MAFA and			
CC	human truncated MAFA, and polynucleotides encoding them, can be			
CC	used in methods for the treatment of inflammatory and allergic			
CC	diseases (e.g. rheumatoid arthritis and asthma), and tumour growth.			
XX				
SQ	Sequence 188 AA:			
	Query Match 51.4%; Score 525.5; DB 20; Length 188;			
	Best Local Similarity 53.5%; Pred.No.1.2e-46;			
	Matches 100; Conservative 29; Mismatches 57; Indels 1; Gaps 1.			
OY	1 MHDSIVYSMLERPTQAONDYGPOKSSSKSPSCSCLVAITLGLTANLLSVILYQWL 60     :             :   :   :   :         :   :			
Db	1 madnslystlelpaaprvgddsrwkvkavlhpcvsvlymvalgillvlmsillyqrfl 60     :             :   :   :   :         :   :			
OY	61 CGGSNYSTCASCPGDPDMKKGNICYYFSVEEKMNNSLEFCLARDSHILVTTNQES 120     :             :   :   :   :         :   :			
Db	61 ccgskgfmcsgscrcpnllwmrnngshcyfsmekrtwnaslkccadqgnllltfpdngvn 120     :             :   :   :   :         :   :			
OY	121 LLOVLSEAFCHIGIRNNSGRMWDGSLPNSRISNSRFVOTCGAINKGLDASSCEVPL 180     :             :   :   :   :         :   :			
Db	121 lfgeyvgedfwygidrididgwrmwedgapalsls-llsnsvvgkcgtlhcrgclhassceval 179     :             :   :   :   :         :   :			
OY	181 HGVCCKV 187			
Db	180 gwicckv 186			

AAE11761	standard; Protein; 168 AA.
AC	AAE11761;
AD	18-DEC-2001 (first entry)
AE	Rat mast cell function associated antigen (MAFA) protein.
AF	Rat; Pharmaceutical composition; mast cell function associated antigen;
AG	MAFA; natural killer cell; NK; tumour; therapy; cytotoxic T-cell; CTL;
AH	immunosuppressive; cytostatic.
AI	Rattus norvegicus.
AJ	WO200170805-A2.
AK	27-SEP-2001.
AL	16-MAR-2001; 2001WO-US08596.
AM	17-MAR-2000; 2000US-190716P.
AN	(GEMI-) GEMINI SCI INC.
AO	Takahashi N, Miyayama T;
AP	WPI: 2001-611482/70.
AQ	DR N-PSDB; AAD18736.
AR	Pharmaceutical composition for treating tumor by stimulating cytotoxic
AS	activity of natural killer cell or T-cell, comprises an agent that
AT	binds to mast cell function-associated antigen ligand on target cell
AW	Example 1; Page 19; 49pp; English.
AX	The present invention relates to a pharmaceutical composition comprising
AY	an agent which specifically binds to a mast cell function associated
AZ	antigen (MAFA) ligand on a target cell, and prevents or inhibits natural
BA	killer (NK)- or T-cell-expressed cell surface MAFA from binding to MAFA
BB	ligand and a pharmaceutically acceptable excipient. The invention is
BC	useful for inhibiting an NK- or a T-cell-expressed cell surface MAFA
BD	binding to a ligand on a target cell, by contacting the pharmaceutical
BE	composition in vitro, ex vivo or in vivo by administering the composition
BF	to the subject, to NK or T-cell or the target cell e.g. tumour cell, in
BG	an amount sufficient to inhibit cell surface MAFA binding to the ligand
BH	on the target cell. The agent or the composition is useful for treating a
BI	tumour by stimulating the cytotoxic activity of an NK cell or a cytotoxic
BJ	T-cell (CTL), where the tumour comprises an NK cell- or CTL-susceptible
BK	tumour cell. The invention is also useful for inhibiting an activity of
BL	NK cell or a T-cell. The present sequence is rat MAFA protein.
BM	Sequence 168 AA;

	Query Match	51.4%;	Score 525.5;	DB 22;	Length 168;	
	Best Local Similarity	53.5%;	Pred. 1.2e-46;			
	Matches 100;	Conservative 29;	Mismatches 57;	Indels 1;	Gaps 1.	
OY	1	MTDSVYSMLELPATQANDYGPOOKSSSKSPSCSLVATITGLTAVLLSVLYQMIL	60			
		:   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :				
Dd	1	madsuisytlepaaprvqddsrwkvkavlnhpccvsvlwmvalgiltvlwmslllygrfl	60			
OY	61	CQGSNYSTCASCPCSPDWMKTKGNHCYCFYSVEDEKMWNSSLFELFCALRDSHLVITPNOEWS	120			
		:   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :				
Dd	61	cqgsqfmcsgscrcspnlwmrngshncylfsmekrdwnsslkfcadksghllffpdngyn	120			
OY	121	LLOYLSEAFWICIGIRNNSGMWREDEGSPLENERISSNVSQCGAILKKNGCLASSCEVL	180			
		:   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :				
Dd	121	lfgeyvgedfyglrtldldgwmedgpalsls-ltsnsvydgcgctchrcgllnassceval	179			
OY	181	HGVCKV 187				
		: : :				

DB	180	gwickcv	186
	RESULT	8	
	AAW88267		
ID	AAW88267	standard; Protein:	99 AA.
XX			
AC	AAW88267;		
XX			
DT	29-MAR-1999	(first entry)	
XX			
DE	Human MAFA splice variant huMAFA(E3/4-).		
XX			
XX	Mast cell function-associated antigen; MAFA; huMAFA(E3/4-);		
KM	splice variant; human; inflammation; allergy; asthma;		
KW	rheumatoid arthritis; tumour; therapy.		
KX			
OS	Homo sapiens.		
PX			
PN	WO9854209-A2.		
XX			
PD	03-DEC-1998.		
XX			
PF	29-MAY-1998; 98WO-GBO1572.		
XX			
PR	31-MAY-1997; 97GB-0011148.		
XX			
PA	(PEPT-) PEPTIDE THERAPEUTICS LTD.		
XX			
PI	Hewitt EL, Lamers MBAC, Lamont A, Williams DH;		
XX			
DR	WPI; 1999-059806/05.		
DR	N-PSDB; AAW84200.		
XX			
PT	New polypeptide having a sequence corresponding to human mast cell		
PT	function associated antigen - useful in forming and manufacturing		
PT	pharmaceutical compositions in the treatment of inflammatory and		
PT	allergic diseases, and tumour growth		
XX			
PPS	Disclosure: Fig 3; 44pp: English.		
XX			
CC	This is the amino acid sequence of human mast cell function-		
CC	associated antigen (MAFA) splice variant huMAFA(E3/4-), which		
CC	lacks the C-lectin-like domain of human MAFA (see AAW88265) but		
CC	retains the intracellular and transmembrane domains as well as the		
CC	extracellular C-terminal tail. Truncated MAFA polypeptides		
CC	including huMAFA(E3/4-), and polynucleotides encoding them, as		
CC	well as synthetic peptides (see AAW88258-64, AAW88268-72), can be used		
CC	be used in compositions for the treatment of inflammatory and		
CC	allergic diseases (e.g. rheumatoid arthritis and asthma), or tumour		
CC	growth.		
XX			
SQ	Sequence	99 AA;	

	Query Match	Similarity	42.1%	Score 431	DB 20	Length 99	
	Best Local	Similarity	50.3%	Pred. No. 3.5e-37			
	Matches	95: Conservative	1:	Mismatches	5:	Indels	90: Gaps
QY	1	MTDSVIYSMLLEPTATQAONDYGPQOKSSSKPSCSCI	VAITGLLTAVALLSVLLYOMIL	60			
Db	1	mtdsviysmlleptatqandypqpksssrpsccscl	valatlglltvalisvlllyqwl	60			
QY	61	CGSGSYSTCASCPCSPDRMKRYGNHCYFSEVEEKDMNSL	LEFCILARDSHLITDQEMS	120			
Db	61	cqg					63
QY	121	LLQVFLSEAFPCMIGLRNNSGWRWEDGSP	LNFSTRSSNFVOTCGA	INKNGLOASCEVPL	180		
Db	64						
QY	181	HGVCKKVRLL	189				



KM cytostatic; gene therapy; vaccine; metastasis.  
 XX Homo sapiens.  
 OS  
 XX MO200157182-A2.  
 PN  
 XX  
 PD 09-AUG-2001.  
 XX  
 PF 17-JAN-2001; 2001MO-US01354.  
 XX  
 XX 31-JAN-2000; 2000US-0179065.  
 PR 04-FEB-2000; 2000US-0180628.  
 PR 24-FEB-2000; 2000US-0184664.  
 PR 02-MAR-2000; 2000US-0186350.  
 PR 16-MAR-2000; 2000US-0189874.  
 PR 17-MAR-2000; 2000US-0190076.  
 PR 18-APR-2000; 2000US-0198123.  
 PR 19-MAY-2000; 2000US-0205515.  
 PR 07-JUN-2000; 2000US-0209467.  
 PR 28-JUN-2000; 2000US-0214886.  
 PR 30-JUN-2000; 2000US-0215135.  
 PR 07-JUL-2000; 2000US-0216647.  
 PR 11-JUL-2000; 2000US-0217487.  
 PR 11-JUL-2000; 2000US-0217496.  
 PR 14-JUL-2000; 2000US-0218290.  
 PR 26-JUL-2000; 2000US-0220963.  
 PR 26-JUL-2000; 2000US-0220964.  
 PR 14-AUG-2000; 2000US-0224518.  
 PR 14-AUG-2000; 2000US-0224519.  
 PR 14-AUG-2000; 2000US-0225213.  
 PR 14-AUG-2000; 2000US-0225214.  
 PR 14-AUG-2000; 2000US-0225266.  
 PR 14-AUG-2000; 2000US-0225267.  
 PR 14-AUG-2000; 2000US-0225268.  
 PR 14-AUG-2000; 2000US-0225270.  
 PR 14-AUG-2000; 2000US-0225447.  
 PR 14-AUG-2000; 2000US-0225757.  
 PR 14-AUG-2000; 2000US-0225758.  
 PR 14-AUG-2000; 2000US-0225759.  
 PR 18-AUG-2000; 2000US-0226279.  
 PR 22-AUG-2000; 2000US-0226681.  
 PR 22-AUG-2000; 2000US-0226688.  
 PR 22-AUG-2000; 2000US-0227182.  
 PR 23-AUG-2000; 2000US-0227009.  
 PR 30-AUG-2000; 2000US-0228924.  
 PR 01-SEP-2000; 2000US-0229287.  
 PR 01-SEP-2000; 2000US-0229343.  
 PR 01-SEP-2000; 2000US-0229344.  
 PR 01-SEP-2000; 2000US-0229345.  
 PR 05-SEP-2000; 2000US-0229509.  
 PR 05-SEP-2000; 2000US-0229513.  
 PR 06-SEP-2000; 2000US-0230437.  
 PR 06-SEP-2000; 2000US-0230438.  
 PR 08-SEP-2000; 2000US-0231242.  
 PR 08-SEP-2000; 2000US-0231243.  
 PR 08-SEP-2000; 2000US-0231244.  
 PR 08-SEP-2000; 2000US-0231413.  
 PR 08-SEP-2000; 2000US-0231414.  
 PR 08-SEP-2000; 2000US-0232080.  
 PR 08-SEP-2000; 2000US-0232081.  
 PR 12-SEP-2000; 2000US-0231968.  
 PR 14-SEP-2000; 2000US-0232397.  
 PR 14-SEP-2000; 2000US-0232398.  
 PR 14-SEP-2000; 2000US-0232399.  
 PR 14-SEP-2000; 2000US-0232400.  
 PR 14-SEP-2000; 2000US-0232401.  
 PR 14-SEP-2000; 2000US-0233063.  
 PR 14-SEP-2000; 2000US-0233064.  
 PR 14-SEP-2000; 2000US-0233065.  
 PR 21-SEP-2000; 2000US-0234223.  
 PR 21-SEP-2000; 2000US-0234274.  
 PR 25-SEP-2000; 2000US-0234997.

PR 25-SEP-2000; 2000US-0234998.  
 PR 26-SEP-2000; 2000US-0235484.  
 PR 27-SEP-2000; 2000US-0235834.  
 PR 27-SEP-2000; 2000US-0235836.  
 PR 29-SEP-2000; 2000US-0236327.  
 PR 29-SEP-2000; 2000US-0236367.  
 PR 29-SEP-2000; 2000US-0236368.  
 PR 29-SEP-2000; 2000US-0236369.  
 PR 29-SEP-2000; 2000US-0236370.  
 PR 02-OCT-2000; 2000US-0236802.  
 PR 02-OCT-2000; 2000US-0237037.  
 PR 02-OCT-2000; 2000US-0237038.  
 PR 02-OCT-2000; 2000US-0237039.  
 PR 02-OCT-2000; 2000US-0237040.  
 PR 13-OCT-2000; 2000US-0239935.  
 PR 13-OCT-2000; 2000US-0239937.  
 PR 20-OCT-2000; 2000US-0240960.  
 PR 20-OCT-2000; 2000US-0241221.  
 PR 20-OCT-2000; 2000US-0241785.  
 PR 20-OCT-2000; 2000US-0241786.  
 PR 20-OCT-2000; 2000US-0241787.  
 PR 20-OCT-2000; 2000US-0241808.  
 PR 20-OCT-2000; 2000US-0241809.  
 PR 20-OCT-2000; 2000US-0241826.  
 PR 01-NOV-2000; 2000US-0244617.  
 PR 08-NOV-2000; 2000US-0246474.  
 PR 08-NOV-2000; 2000US-0246475.  
 PR 08-NOV-2000; 2000US-0246476.  
 PR 08-NOV-2000; 2000US-0246477.  
 PR 08-NOV-2000; 2000US-0246478.  
 PR 08-NOV-2000; 2000US-0246523.  
 PR 08-NOV-2000; 2000US-0246524.  
 PR 08-NOV-2000; 2000US-0246525.  
 PR 08-NOV-2000; 2000US-0246526.  
 PR 08-NOV-2000; 2000US-0246527.  
 PR 08-NOV-2000; 2000US-0246528.  
 PR 08-NOV-2000; 2000US-0246532.  
 PR 08-NOV-2000; 2000US-0246609.  
 PR 08-NOV-2000; 2000US-0246610.  
 PR 08-NOV-2000; 2000US-0246611.  
 PR 08-NOV-2000; 2000US-0246613.  
 PR 17-NOV-2000; 2000US-0249207.  
 PR 17-NOV-2000; 2000US-0249208.  
 PR 17-NOV-2000; 2000US-0249209.  
 PR 17-NOV-2000; 2000US-0249210.  
 PR 17-NOV-2000; 2000US-0249211.  
 PR 17-NOV-2000; 2000US-0249212.  
 PR 17-NOV-2000; 2000US-0249213.  
 PR 17-NOV-2000; 2000US-0249214.  
 PR 17-NOV-2000; 2000US-0249215.  
 PR 17-NOV-2000; 2000US-0249216.  
 PR 17-NOV-2000; 2000US-0249217.  
 PR 17-NOV-2000; 2000US-0249218.  
 PR 17-NOV-2000; 2000US-0249244.  
 PR 17-NOV-2000; 2000US-0249245.  
 PR 17-NOV-2000; 2000US-0249264.  
 PR 17-NOV-2000; 2000US-0249265.  
 PR 17-NOV-2000; 2000US-0249297.  
 PR 17-NOV-2000; 2000US-0249299.  
 PR 17-NOV-2000; 2000US-0249300.  
 PR 01-DEC-2000; 2000US-0250160.  
 PR 01-DEC-2000; 2000US-0250391.  
 PR 05-DEC-2000; 2000US-0251030.  
 PR 05-DEC-2000; 2000US-0251988.  
 PR 05-DEC-2000; 2000US-0256719.  
 PR 06-DEC-2000; 2000US-0251479.  
 PR 08-DEC-2000; 2000US-0251856.  
 PR 08-DEC-2000; 2000US-0251868.  
 PR 08-DEC-2000; 2000US-0251869.  
 PR 08-DEC-2000; 2000US-0251989.  
 PR 08-DEC-2000; 2000US-0251990.  
 PR 11-DEC-2000; 2000US-0254097.  
 PR 05-JAN-2001; 2001US-0259678.



[illegible]

PR		11-DEC-2000; 2000US-0254097.
PR		05-JAN-2001; 2001US-0259678.
XX		(HUMA-) HUMAN GENOME SCI INC.
PA	Rosen CA,	Barash SC, Ruben SM;
PI	WPI; 2001-465572/50.	
XX	N-PsDB; AAS31391.	
DR		
PT		
PS		
Pt		
XX		
CC	Claim 11; SEQ ID No 470; 577pp; English.	
CC	The invention relates to isolated nucleic acid molecules encoding novel human secreted extracellular matrix proteins (SPS). The polynucleotides and proteins are used to prevent, treat a medical condition, in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. For example, disorders associated with decreased expression of SPS. The SP polynucleotide or a vector expressing them may be administered to treat diseases by gene therapy. Antisense molecules may be administered to down regulate expression of SPS by binding with the cells own genes and preventing their expression. The polynucleotides can also be used as DNA probes in diagnostic assays. The SPS may also be used as antigens to produce antibodies and to identify modulators (agonists and antagonists) of the SPS. The anti-(SP) antibodies and CC antagonists may also be used to down regulate expression and activity of SPS and as diagnostic agents for detecting the presence of SPS in samples. The disorders include for example: Immune/autoimmune diseases (e.g. HIV (human immunodeficiency virus), infections, anaemia, rheumatoid arthritis and multiple sclerosis), cancers and hyperproliferative disorders (e.g. melanomas, neoplasms of the breast or liver, Sezary syndrome and Gaucher's disease), neurological diseases (e.g. Alzheimer's disease, Parkinson's disease) cardio-/cerebrovascular disorders (e.g. cardiac arrest, tachycardia and angina), infections caused by bacteria, viruses and fungi and ocular disorders (e.g. corneal infections). Other uses CC include wound healing, maintenance of organs before transplantation,	
Query Match	Best Local Similarity	Score 226; DB 22; Length 198; Matches 58; Conservative 27; Mismatches 53; Indels 48; Gaps 8;
OY	44 GLTFLVLTSLVLY--QWLTV-COG-----SNYSRCACSPS	74   :   :   :   :   :   :   :   :   :   :   :   :   : 16 gllctlttlstlllvsvsgvllkcygyscanatqyedtdqlxvmngtrlnistnkcdlatcra
Dd	75 -----CPDPMKMGYNHCYYFSEVEREDMNSLLEPCILARDSHLLVTVDNQEMSLLOVFSEA	129   :   :   :   :   :   :   :   :   :   :   :   :   : 76 dqtvtgcgevwlkkyggkkcyfswemskwsdsyyvlletkshtlllhqdlemafidknlrtql
Oy	130 -FCWTGLERNNS---GMRREDGSPLNFSRISNSNVQ-----TCGAINKNGLAASSCEVP	179   :   :   :   :   :   :   :   :   :   :   :   :   : Db 136 nywvatgnlfitslkmrlwtvdgspld----skflfikgpakenscaalkesklfselctssv
OY	180 LHWCK 185	191
Dd	192 fkwldq 197	
RESULT 13	AUO19659 standard; Protein; 203 AA.	
ID	AAU19659	
AC	AAU19659;	
XX		
DT	04-DEC-2001 (first entry)	
DE	Human novel extracellular matrix protein, Seq ID NO 309.	
KW	Human; secreted extracellular matrix protein; immunomodulatory;	
XV	Anti-IHV; antianemic; antirheumatic; antisclerotic; cardiant; vascular;	

KW cerebroprotective; thrombolytic; antimicrobial; ophthalmic; cytostatic;  
KW antialzheimers; immune/autoimmune disease; HIV infection; anaemia;  
KW human immunodeficiency virus; rheumatoid arthritis; multiple sclerosis;  
KW cancers; hyperproliferative disorder; breast neoplasm; melanoma;  
KW Sezary syndrome; Gaucher's disease; neurological diseases;  
KW Alzheimer's disease; Parkinson's disease; cardiovascular disorder;  
KW cardiac arrest; tachycardia; angina; infection; corneal infections;  
KW wound healing; immunogen; gene therapy; antisense; food additive.  
XX  
OS Homo sapiens.  
XX  
PN WO20015368-A1.  
XX  
PD 02-AUG-2001.  
XX  
PF 17-JAN-2001; 2001WO-US01348.  
XX  
PR 31-JAN-2000; 2000US-0179065.  
PR 04-FEB-2000; 2000US-0180628.  
PR 24-FEB-2000; 2000US-0184664.  
PR 02-MAR-2000; 2000US-0186350.  
PR 16-MAR-2000; 2000US-0189874.  
PR 17-MAR-2000; 2000US-0190076.  
PR 18-APR-2000; 2000US-0198123.  
PR 19-MAY-2000; 2000US-0205515.  
PR 07-JUN-2000; 2000US-0209467.  
PR 28-JUN-2000; 2000US-0214886.  
PR 30-JUN-2000; 2000US-0215135.  
PR 07-JUL-2000; 2000US-0216647.  
PR 07-JUL-2000; 2000US-0216880.  
PR 11-JUL-2000; 2000US-0217487.  
PR 11-JUL-2000; 2000US-0217496.  
PR 14-JUL-2000; 2000US-0218290.  
PR 26-JUL-2000; 2000US-0220963.  
PR 26-JUL-2000; 2000US-0220964.  
PR 14-AUG-2000; 2000US-0224518.  
PR 14-AUG-2000; 2000US-0224519.  
PR 14-AUG-2000; 2000US-0225213.  
PR 14-AUG-2000; 2000US-0225214.  
PR 14-AUG-2000; 2000US-0225266.  
PR 14-AUG-2000; 2000US-0225267.  
PR 14-AUG-2000; 2000US-0225268.  
PR 14-AUG-2000; 2000US-0225270.  
PR 14-AUG-2000; 2000US-0225447.  
PR 14-AUG-2000; 2000US-0225757.  
PR 14-AUG-2000; 2000US-0225758.  
PR 14-AUG-2000; 2000US-0225759.  
PR 18-AUG-2000; 2000US-0226279.  
PR 22-AUG-2000; 2000US-0226681.  
PR 22-AUG-2000; 2000US-0226868.  
PR 23-AUG-2000; 2000US-0227182.  
PR 23-AUG-2000; 2000US-0227009.  
PR 30-AUG-2000; 2000US-0228924.  
PR 01-SEP-2000; 2000US-0229287.  
PR 01-SEP-2000; 2000US-0229343.  
PR 01-SEP-2000; 2000US-0229344.  
PR 01-SEP-2000; 2000US-0229345.  
PR 05-SEP-2000; 2000US-0229509.  
PR 05-SEP-2000; 2000US-0229513.  
PR 06-SEP-2000; 2000US-0230437.  
PR 06-SEP-2000; 2000US-0230438.  
PR 08-SEP-2000; 2000US-0231242.  
PR 08-SEP-2000; 2000US-0231243.  
PR 08-SEP-2000; 2000US-0231244.  
PR 08-SEP-2000; 2000US-0231413.  
PR 08-SEP-2000; 2000US-0231414.  
PR 08-SEP-2000; 2000US-0232080.  
PR 08-SEP-2000; 2000US-0232081.  
PR 12-SEP-2000; 2000US-0231968.  
PR 14-SEP-2000; 2000US-0233397.  
PR 14-SEP-2000; 2000US-0233398.  
PR 14-SEP-2000; 2000US-0233399.  
PR 14-SEP-2000; 2000US-0232400.  
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PR 14-SEP-2000; 2000US-0232401.  
PR 14-SEP-2000; 2000US-0233063.  
PR 14-SEP-2000; 2000US-0233064.  
PR 14-SEP-2000; 2000US-0233065.  
PR 21-SEP-2000; 2000US-0234223.  
PR 21-SEP-2000; 2000US-0234274.  
PR 25-SEP-2000; 2000US-0234997.  
PR 25-SEP-2000; 2000US-0234998.  
PR 26-SEP-2000; 2000US-0235484.  
PR 27-SEP-2000; 2000US-0235834.  
PR 27-SEP-2000; 2000US-0235836.  
PR 29-SEP-2000; 2000US-0236327.  
PR 29-SEP-2000; 2000US-0236367.  
PR 29-SEP-2000; 2000US-0236368.  
PR 29-SEP-2000; 2000US-0236369.  
PR 29-SEP-2000; 2000US-0236370.  
PR 02-OCT-2000; 2000US-0236802.  
PR 02-OCT-2000; 2000US-0237037.  
PR 02-OCT-2000; 2000US-0237038.  
PR 02-OCT-2000; 2000US-0237039.  
PR 02-OCT-2000; 2000US-0237040.  
PR 13-OCT-2000; 2000US-0239935.  
PR 13-OCT-2000; 2000US-0239937.  
PR 20-OCT-2000; 2000US-0240960.  
PR 20-OCT-2000; 2000US-0241221.  
PR 20-OCT-2000; 2000US-0241785.  
PR 20-OCT-2000; 2000US-0241786.  
PR 20-OCT-2000; 2000US-0241787.  
PR 20-OCT-2000; 2000US-0241808.  
PR 20-OCT-2000; 2000US-0241809.  
PR 20-OCT-2000; 2000US-0241826.  
PR 01-NOV-2000; 2000US-0244617.  
PR 08-NOV-2000; 2000US-0246474.  
PR 08-NOV-2000; 2000US-0246475.  
PR 08-NOV-2000; 2000US-0246476.  
PR 08-NOV-2000; 2000US-0246477.  
PR 08-NOV-2000; 2000US-0246478.  
PR 08-NOV-2000; 2000US-0246523.  
PR 08-NOV-2000; 2000US-0246524.  
PR 08-NOV-2000; 2000US-0246525.  
PR 08-NOV-2000; 2000US-0246526.  
PR 08-NOV-2000; 2000US-0246527.  
PR 08-NOV-2000; 2000US-0246528.  
PR 08-NOV-2000; 2000US-0246532.  
PR 08-NOV-2000; 2000US-0246609.  
PR 08-NOV-2000; 2000US-0246610.  
PR 08-NOV-2000; 2000US-0246611.  
PR 08-NOV-2000; 2000US-0246613.  
PR 17-NOV-2000; 2000US-0249207.  
PR 17-NOV-2000; 2000US-0249208.  
PR 17-NOV-2000; 2000US-0249209.  
PR 17-NOV-2000; 2000US-0249210.  
PR 17-NOV-2000; 2000US-0249211.  
PR 17-NOV-2000; 2000US-0249212.  
PR 17-NOV-2000; 2000US-0249213.  
PR 17-NOV-2000; 2000US-0249214.  
PR 17-NOV-2000; 2000US-0249215.  
PR 17-NOV-2000; 2000US-0249216.  
PR 17-NOV-2000; 2000US-0249217.  
PR 17-NOV-2000; 2000US-0249218.  
PR 17-NOV-2000; 2000US-0249244.  
PR 17-NOV-2000; 2000US-0249245.  
PR 17-NOV-2000; 2000US-0249264.  
PR 17-NOV-2000; 2000US-0249265.  
PR 17-NOV-2000; 2000US-0249297.  
PR 17-NOV-2000; 2000US-0249299.  
PR 17-NOV-2000; 2000US-0249300.  
PR 01-DEC-2000; 2000US-0250160.  
PR 01-DEC-2000; 2000US-0250391.  
PR 05-DEC-2000; 2000US-0251030.  
PR 05-DEC-2000; 2000US-0251988.  
PR 05-DEC-2000; 2000US-0256719.  
PR 06-DEC-2000; 2000US-0251479.





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OM protein - protein search, using sw model

Run on: September 9, 2002, 14:59:46 : Search time 27.34 Seconds  
(Without alignments)  
1195.905 Million cell updates/sec

Title: US-09-811-367b-1  
Perfect score: 1023  
Sequence: 1 MTDSVIYSMLPTAQAON.....GLQASSCEVPLHGVCAYRL 189

Scoring table:  
BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 562222 seqs, 172994929 residues  
Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

SPTREMBL\_19:\*  
1: sp-archaea:\*  
2: sp-bacteria:\*  
3: sp-fungi:\*  
4: sp-human:\*  
5: sp-invertebrate:\*  
6: sp-mammal:\*  
7: sp-mhc:\*  
8: sp-organelle:\*  
9: sp-phage:\*  
10: sp-plant:\*  
11: sp-rodent:\*  
12: sp-virus:\*  
13: sp-vertebrate:\*  
14: sp-unclassified:\*  
15: sp-virus:\*  
16: sp-bacteriap:\*  
17: sp-atcheap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1023	100.0	189	4	043198
2	1007	98.4	189	4	075613
3	994	97.2	195	4	096E93
4	548.5	53.6	188	11	088713
5	525.5	51.4	188	11	064335
6	226	22.1	231	4	09M252
7	225	22.0	181	4	09M251
8	219.5	21.5	275	11	09D403
9	210	20.5	227	11	09M132
10	210	20.5	231	11	054872
11	203	19.8	233	6	095M15
12	201.5	19.7	231	6	09M2K3
13	201	19.6	225	4	012918
14	199.5	19.5	180	6	09M2K8
15	199.5	19.5	231	6	09GK88
16	199.5	19.5	269	11	Q9D676

17	199	19.5	233	6	09MVM6	09mvm6 pan troglod
18	198.5	19.4	179	6	09M2K9	09m2k9 macaca mula
19	198.5	19.4	179	6	09GK91	09gk91 macaca mula
20	197	19.3	180	4	043773	043773 homo sapien
21	197	19.3	232	11	054709	054709 mus musculu
22	196.5	19.2	246	6	09M2K2	09m2k2 macaca mula
23	196	19.2	211	11	0912W5	0912w5 mus musculu
24	196	19.2	246	6	09M2K1	09m2k1 macaca mula
25	195.5	19.1	244	11	092202	092202 mus musculu
26	195.5	19.1	278	6	09XTA8	09xta8 oryctolaqus
27	194.5	19.0	178	11	0912W9	0912w9 mus musculu
28	194.5	19.0	179	6	09M2A1	09m2a1 pan troglod
29	193	18.9	257	13	090636	090636 gallus gall
30	193	18.9	270	6	P79391	P79391 bos taurus
31	192.5	18.8	208	11	0912W7	0912w7 mus musculu
32	192.5	18.8	244	11	09M031	09m031 mus musculu
33	192	18.8	236	6	095194	095194 macaca mula
34	191.5	18.7	230	11	054871	054871 rattus norv
35	191	18.7	148	6	09M2K7	09m2k7 macaca mula
36	190	18.6	199	6	095M01	095m01 bos taurus
37	190	18.6	227	11	061973	061973 mus musculu
38	189	18.5	226	6	09M239	09m239 pan troglod
39	188	18.4	124	4	09UBQ0	09ubq0 homo sapien
40	188	18.4	148	4	043321	043321 homo sapien
41	188	18.4	231	4	09NR42	09nr42 homo sapien
42	187.5	18.3	231	6	09M2K5	09m2k5 macaca mula
43	187.5	18.3	238	11	0912X1	0912x1 mus musculu
44	187	18.3	179	11	035778	035778 rattus norv
45	187	18.3	231	6	09M238	09m238 pan troglod

#### ALIGNMENTS

RESULT 1  
ID 043198 PRELIMINARY; PRT; 189 AA.  
AC 043198;  
DT 01-JUN-1998 (TEMBLrel. 06, Created)  
DT 01-JUN-1998 (TEMBLrel. 06, Last sequence update)  
DT 01-DEC-2001 (TEMBLrel. 19, Last annotation update)  
DE MAST CELL FUNCTION-ASSOCIATED ANTIGEN.  
GN MAF.  
OS Homo sapiens (human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE-ENZYMIC DIGESTED LUNG;  
RX MEDLINE=98438735; PubMed=9765598;  
RA Lamers M.B., Lamont A.G., Williams D.H.;  
RT "Human MAF has alternatively spliced variants";  
RL Biochim. Biophys. Acta 1399:209-212(1998).  
DR EMBL: AF034952; AAC34731.1; .  
DR HSSP: P06734; IHLT.  
DR InterPro: IPR001304; lectin\_c.  
DR Pfam: PF00059; lectin\_c; 1.  
DR SMART: SM00034; CLECT. 1.  
DR PROSITE: PS50041; C\_TYPE\_LECTIN\_2; 1.  
SQ SEQUENCE 189 AA; 21079 MW; 15E042AD40B2BAF6 CRC64;

Query Match 100.0%; Score 1023; DB 4; Length 189;  
Best Local Similarity 100.0%; Pred. No. 7.5e-105;  
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTDSVIYSMLPTAQAONDYGPQOKSSSKSPSCGLVAITGLTLAVLLSVLYQWIL 60  
DB 1 MTDSVIYSMLPTAQAONDYGPQOKSSSKSPSCGLVAITGLTLAVLLSVLYQWIL 60  
QY 61 CGSNSTGASCPSCPDNWKYGNHCYYSVEKDMNSSLFCLARDSHLLVTNDQMS 120

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Db 61 COG5N1STCASCPCPDMMKTKGNHCYFVSVEKDMNSLFCCLARDSHLVTITDQEMS 120
QY 121 LLOVFLSEAFWCIGILRNNSGWRMEDGSPINFSRISNSFVOTCGAINKNGLOASSCEVPL 180
Db 121 LLOVFLSEAFWCIGILRNNSGWRMEDGSPINFSRISNSFVOTCGAINKNGLOASSCEVPL 180
QY 181 HGVCCKKRL 189
Db 181 HGVCCKKRL 189

RESULT 2
075613 PRELIMINARY; PRT; 189 AA.
AC 075613;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE ITIM-CONTAINING RECEPTOR MAFA-L.
CN MAFA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Butcher S., Arney K.L., Cook G.P.;
RT "MAFA-L, an ITIM-containing receptor encoded by the human NK cell gene
RT complex and expressed by basophils and NK cells.";
RL Eur. J. Immunol. 28:0-0(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE-99077194; PubMed-9862378;
RA Hanke T., Corral L., Vance R.E., Raulat D.H.;
RT "2F1 antigen, the mouse homolog of the rat '31', is a lectin-like type
RT II transmembrane receptor expressed by natural killer cells.";
RL Eur. J. Immunol. 28:4409-4417(1998).
DR EMBL; AF081675; AAC32200.1; -.
DR HSSP; P06734; 1H1.
DR InterPro; IPR001304; lectin_C.
DR Pfam; PF00059; lectin_C.1.
DR SMART; SM00034; CLECT.1.
DR PROSITE; PS50041; C_Type_Lectin_2; 1.
SQ SEQUENCE 189 AA; 21206 MW; FA9023F1523656A8 CRC64;

Query Match 98.4%; Score 1007; DB 4; Length 189;
Best Local Similarity 98.4%; Pred. No. 4.3e-103;
Matches 186; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 MTDVITYSMLELPTATQANDYGPQOKSSSKPSCCLVAITLGLTAVLLSVLYQWIL 60
Db 1 MTDVITYSMLELPTATQANDYGPQOKSSSKPSCCLVAITLGLTAVLLSVLYQWIL 60
QY 61 COG5N1STCASCPCPDMMKTKGNHCYFVSVEKDMNSLFCCLARDSHLVTITDQEMS 120
Db 61 COG5N1STCASCPCPDMMKTKGNHCYFVSVEKDMNSLFCCLARDSHLVTITDQEMS 120
QY 121 LLOVFLSEAFWCIGILRNNSGWRMEDGSPINFSRISNSFVOTCGAINKNGLOASSCEVPL 180
Db 121 LLOVFLSEAFWCIGILRNNSGWRMEDGSPINFSRISNSFVOTCGAINKNGLOASSCEVPL 180
QY 181 HGVCCKKRL 189
Db 181 HGVCCKKRL 189

RESULT 3
096E93 PRELIMINARY; PRT; 195 AA.
AC 096E93;
DT 01-DEC-2001 (TREMBlrel. 19, Created)

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DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE SIMILAR TO KILLER CELL LECTIN-LIKE RECEPTOR SUBFAMILY G, MEMBER
DE 1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BONE MARROW, AND ACUTE MYELOCYTIC LEUKEMIA;
RA Strausberg R.;
RL Submitted (AUG-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; BC012621; AAH12621.1; -.
KW Receptor; Lectin.
SQ SEQUENCE 195 AA; 21831 MW; 178E98E08EBC473 CRC64;

Query Match 97.2%; Score 994; DB 4; Length 195;
Best Local Similarity 98.4%; Pred. No. 1.2e-101;
Matches 183; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 MTDVITYSMLELPTATQANDYGPQOKSSSKPSCCLVAITLGLTAVLLSVLYQWIL 60
Db 1 MTDVITYSMLELPTATQANDYGPQOKSSSKPSCCLVAITLGLTAVLLSVLYQWIL 60
QY 61 COG5N1STCASCPCPDMMKTKGNHCYFVSVEKDMNSLFCCLARDSHLVTITDQEMS 120
Db 61 COG5N1STCASCPCPDMMKTKGNHCYFVSVEKDMNSLFCCLARDSHLVTITDQEMS 120
QY 121 LLOVFLSEAFWCIGILRNNSGWRMEDGSPINFSRISNSFVOTCGAINKNGLOASSCEVPL 180
Db 121 LLOVFLSEAFWCIGILRNNSGWRMEDGSPINFSRISNSFVOTCGAINKNGLOASSCEVPL 180
QY 181 HGVCCKKRL 186
Db 181 HGVCCKKRL 186

RESULT 4
088713 PRELIMINARY; PRT; 188 AA.
AC 088713;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-AUG-1999 (TREMBlrel. 11, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE MASP CELL FUNCTION-ASSOCIATED ANTIGEN 2F1 (MAFA) (KILLER CELL
DE LECTIN-LIKE RECEPTOR G1).
GN KIRG1 OR MAFA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C.B-17 SCID;
RX MEDLINE-99077194; PubMed-9862378;
RA Hanke T., Corral L., Vance R.E., Raulat D.H.;
RT "2F1 antigen, the mouse homolog of the rat '31', is a lectin-like type
RT II transmembrane receptor expressed by natural killer cells.";
RL Eur. J. Immunol. 28:4409-4417(1998).
RN [2]
RP SEQUENCE OF 2-188 FROM N.A.
RA Blaser C.;
RL Submitted (SEP-1998) to the EMBL/Genbank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SVEVTAOFBR; TISSUE=SPLEEN;
RX MEDLINE-21115136; PubMed-11220622;
RA Voehringer D., Kaufmann M., Pitscher H.;
RT "Genomic structure, alternative splicing, and physical mapping of the
RT killer cell lectin-like receptor G1 gene (KIRG1), the mouse homologue
RT of MAFA.";

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RL Immunogenetics 52:206-211(2001).  
DR EMBL; AF097357; RAD03718.1; -  
DR EMBL; AJ010751; CA00342.1; -  
DR EMBL; AF317727; AAK4082.1; -  
DR MGD; MGI:1355294; K1rg1.  
DR InterPro: IPR001304; Lectin\_c.  
DR Pfam; PF00059; lectin\_c; 1.  
DR SMART; SM00034; lectin\_c; 1.  
DR PROSITE; PS50041; C\_Type\_Lectin\_2; 1.  
KW Receptor; Lectin  
SQ SEQUENCE 188 AA; 21396 MW; 876336802EA134F1 CRC64;

Query Match 53.6%; Score 548.5; DB 11; Length 188;  
Best Local Similarity 55.6%; Pred. No. 1.6e-52;  
Matches 104; Conservative 26; Mismatches 56; Indels 1; Gaps 1;

QY 1 WDSVIYSMLELPATQAQNDYGPQOKSSSKPSCGLVAITGLTAVLLSVLYQWIL 60  
DB 1 MADSSIVSTLELPAPQVQDESRWKLKAVLHRPHLSRFAVVALGLTILMSLTMQRTL 60  
QY 61 COGSNTSCASCPSPDRMKKYGHCYFFSVEEKDNSSLEFCLARDSHLVTIDNQEMS 120  
DB 61 CCGSKDSTSCSPSCPIWTRNGSHCYFSEMEKDNSSSLKFCADKSHLLTFPDNGYK 120  
QY 121 LQVFLSEAFQWIGLRNNSGMRWEDSGPLNFSRISNSFVOTGAIKNGLOASSCEVPL 180  
DB 121 LFEQYVEDPYWIGLRIDGWRNEDGPAISLILSNVYQKCGTTRHCGILHASSCEVAL 179  
QY 181 HGVCCKV 187  
DB 180 OWICKRV 186

RESULT 5

ID 064335 PRELIMINARY; PRT; 188 AA.

AC 064335;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
DE MAFR PROTEIN.  
GN MAFR.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=SPRAGUE DAWLEY; TISSUE=TESTIS;  
RA Bocek Jr P., Gutmann M.D., Pecht I.;  
RL Submitted (APR-1996) to the EMBL/Genbank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96016176; PubMed=7568140;  
RA Gutmann M.D., Tal M., Pecht I.;  
RT "A secretion inhibitory signal transduction molecule on mast cells is  
another C-type lectin";  
RL Proc. Natl. Acad. Sci. U.S.A. 92:9397-9401(1995).  
DR EMBL; X97191; CA65829.1; -  
DR EMBL; X97192; CA65829.1; JOINED.  
DR EMBL; X97193; CA65829.1; JOINED.  
DR EMBL; X97194; CA65829.1; JOINED.  
DR EMBL; X97195; CA65829.1; JOINED.  
DR EMBL; X79812; CA65829.1; -  
DR InterPro: IPR001304; lectin\_c.  
DR Pfam; PF00059; lectin\_c; 1.  
DR SMART; SM00034; lectin\_c; 1.  
DR PROSITE; PS50041; C\_Type\_Lectin\_2; 1.  
SQ SEQUENCE 188 AA; 21356 MW; 2CC8032D4D020B15 CRC64;

Query Match 51.4%; Score 525.5; DB 11; Length 188;

Best Local Similarity 53.5%; Pred. No. 5.4e-50;  
Matches 100; Conservative 29; Mismatches 57; Indels 1; Gaps 1;

QY 1 WDSVIYSMLELPATQAQNDYGPQOKSSSKPSCGLVAITGLTAVLLSVLYQWIL 60  
DB 1 MADSSIVSTLELPAPQVQDESRWKLKAVLHRPHLSRFAVVALGLTILMSLTMQRTL 60  
QY 61 COGSNTSCASCPSPDRMKKYGHCYFFSVEEKDNSSLEFCLARDSHLVTIDNQEMS 120  
DB 61 CCGSKGFCSCSPSCPIWTRNGSHCYFSEMEKDNSSSLKFCADKSHLLTFPDNGYV 120  
QY 121 LQVFLSEAFQWIGLRNNSGMRWEDSGPLNFSRISNSFVOTGAIKNGLOASSCEVPL 180  
DB 121 LFEQYVEDPYWIGLRIDGWRNEDGPAISLILSNVYQKCGTTRHCGILHASSCEVAL 179  
QY 181 HGVCCKV 187  
DB 180 OWICKRV 186

RESULT 6

ID 09NZS2 PRELIMINARY; PRT; 231 AA.

AC 09NZS2;  
DT 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
DE LECTIN-LIKE RECEPTOR FL (ACTIVATING CORECEPTOR NKp80).  
GN KLRF1 OR ML/KLRF1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20135860; PubMed=10671213;  
RA Roda-Navarro P., Arce I., Renedo M., Montgomery K., Kucherlapati R.,  
RA Fernandez-Puiz E.;  
RT "Human KLRF1, a novel member of the killer cell lectin-like receptor  
gene family: molecular characterization, genomic structure, physical  
mapping to the NK gene complex and expression analysis";  
RL Eur. J. Immunol. 30:568-576(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=LIMPHOID;  
RX MEDLINE=21150889; PubMed=11265639;  
RA Vitale M., Falco M., Castriiconi R., Parolini S., Zambello R.,  
RA Semenzato G., Blassoni R., Bottino C., Moretta L., Moretta A.;  
RT "Identification of NKp80, a novel triggering molecule expressed by  
human natural killer cells";  
RL Eur. J. Immunol. 31:233-242(2001).  
DR EMBL; AF175206; AAF37804.1; -  
DR EMBL; AJ305370; CAC29425.1; -  
DR InterPro: IPR001304; lectin\_c.  
DR Pfam; PF00059; lectin\_c; 1.  
DR SMART; SM00034; lectin\_c; 1.  
DR PROSITE; PS50041; C\_Type\_Lectin\_2; 1.  
KW Receptor.  
SQ SEQUENCE 231 AA; 26562 MW; A2F7BE6D4341AFDE CRC64;

Query Match 22.1%; Score 226; DB 4; Length 231;  
Best Local Similarity 31.2%; Pred. No. 7.4e-17;  
Matches 58; Conservative 27; Mismatches 53; Indels 48; Gaps 8;

QY 44 GLTAVLLSVLY--QWIL--COG-----SNSTSCSCS 74  
DB 49 GLTILFLISLILVLSQGVLLCKGKSCSNATQYEDTGDKLVNNGTRNINSKDLCASTRSA 108  
QY 75 -----CPDRMKKYGHCYFFSVEEKDNSSLEFCLARDSHLVTIDNQMSLQVFLSEA 129  
DB 109 DQTVLCQSEMLKYGCKYWFSEMEKDNSSSLKFCADKSHLLTFPDNGYK 168

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QY 130 -FCWIGLRNNS---GWRWEDGSPLNFRISNSNFVQ-----TCGAINKNGLOASSCEVP 179
DB 169 NYWIGLNTSTSLKMTWTWVDSPID-----SKIFFINGPAKENSACAIFSKIFSTCCSV 224
QY 180 LHVCK 185
DB 225 FKWICQ 230

RESULT 7
Q9NZS1 PRELIMINARY: PRT; 181 AA.
Q9NZS1:
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE LECTIN-LIKE RECEPTOR FL, SPLICE VARIANT 1 KLRFL-S1.
GN KLRFL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxID=9606;
RX MEDLINE-20135860; PubMed-10671213;
RA Roda-Navarro P., Arce I., Renedo M., Montgomery K., Kucherlapati R.,
RA Fernandez-Ruiz E.,
RA "Human KLRFL, a novel member of the killer cell lectin-like receptor
RT gene family: molecular characterization, genomic structure, physical
RT mapping to the NK gene complex and expression analysis.";
RL Eur. J. Immunol. 30:568-576(2000).
DR EMBL: AF175207; AAF37805.1; -
DR InterPro: IPR001304; lectin_c.
DR Pfam: PF00059; lectin_c; 1.
DR SMART: SM00034; CLECT. 1.
DR PROSITE: PS50041; C_TYPE_LECTIN_2; 1.
DR RECEPTOR.
SQ SEQUENCE 181 AA; 21204 MW; 6464240CA1E551 CRC64;

Query Match 22.0%; Score 225; DB 4; Length 181;
Best Local Similarity 33.6%; Pred. No. 7.1e-17;
Matches 51; Conservative 26; Mismatches 45; Indels 30; Gaps 6;

QY 44 GILTAVALSVLYXOMILCGSNSTSCASPCSDRMKGNHCYYSVEKDMNSSLFEC 103
DB 49 GILTLLISLIL- VLCO-----SEWLKYOGKCYFNSNEKKSMSDSVYC 92
QY 104 LARDSLVTYTNQEMSLQVFLSEA-FCWIGLRNNS--GWRWEDGSPLNFRISNSNF 159
DB 93 LERKSHLITIHOLEKAFIOKNIRQLNYVIGLNTSTSLKMTWTWVDSPID---SKIFF 148
QY 160 VO-----TCGAINKNGLOASSCEVPLHGVCK 185
DB 149 IKGPAKENSACAIFSKIFSTCCSVFKWICQ 180

RESULT 8
Q9D403 PRELIMINARY: PRT; 275 AA.
Q9D403:
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE 4933425B16RIK PROTEIN.
GN 4933425B16RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=TESTIS;

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RX MEDLINE-21085660; PubMed-11217851;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishi Y.,
RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana S.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staudli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Barsi G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bona M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamaya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL: AK016908; BAB30491.1; -
DR HSSP: P23807; 11XX.
DR MGD: MGI:1918433; 4933425B16RIK.
DR InterPro: IPR001304; lectin_c.
DR Pfam: PF00059; lectin_c; 1.
DR SMART: SM00034; CLECT. 1.
DR PROSITE: PS50041; C_TYPE_LECTIN_2; 1.
DR SEQUENCE 275 AA; 31360 MW; C9792BA25C9B5CC2 CRC64;

Query Match 21.5%; Score 219.5; DB 11; Length 275;
Best Local Similarity 31.6%; Pred. No. 4.7e-16;
Matches 60; Conservative 34; Mismatches 73; Indels 23; Gaps 9;

QY 16 TQANDYGPQOK--SSSSKPCSCVAITL-GILTAVAL-----LSVLLYOMILCGSNYS 67
DB 79 SOLQKSIHPQDNLSESLNSRSKSTFESLQSGISALLENQEQVATKCEFLIHASDH- 137
QY 68 TCASPCSDRMKGNHCYYSV-EEKWNSSLFECPLARDSLVTYTNQEMSL- QV 124
DB 138 ---KCNPCFKTQWQYSGCYFSINEKKSMSDSRKDCIDKNALVKIDSTEERLLOSQL 194
QY 125 FLSEAFQWIGLR-NNSG--NRWEDG-----PLNFRISNSNFQTCGAINKNGLOASSC 176
DB 195 SLTFSPFWIGLSWNSSGRNLMWEDGSPPTLLSDKELASFGNSRECAFERGNITVSR 254
QY 177 EYPLHGVCK 186
DB 255 RAETPWICK 264

RESULT 9
Q9WU32 PRELIMINARY: PRT; 227 AA.
Q9WU32:
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE NATURAL KILLER CELL RECEPTOR NKGB.
GN KLRCL OR NKGB.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE-99190498; PubMed-10092077;
RA Lohwasser S., Hande P., Mager D.L., Takei F.;
RT "Cloning of murine NKGBA, B and C: second family of C-type lectin
RT receptors on murine NK cells.";
RL Eur. J. Immunol. 29:755-761(1999).

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DR EMBL; AF109784; AAD24970.1; -  
 DR MGD; MG1:1336161; K1rc1.  
 DR InterPro: IPR001304; lectin\_c.  
 DR Pfam: PF00059; lectin\_c; 1.  
 DR SMART; SM00034; CLECT; 1.  
 DR PROSITE; PS50041; C\_TYPE\_LECTIN\_2; 1.  
 DR Receptor.  
 KW SEQUENCE 227 AA; 25746 MW; 1651968539C28C86 CRC64;

Query Match 20.5%; Score 210; DB 11; Length 227;  
 Best Local Similarity 27.1%; Pred. No. 4.2e-15;

Matches 62; Conservative 33; Mismatches 78; Indels 56; Gaps 12;

QY 3 DSVYSLMELPTAQAQNDY-----GPG-----QKSSSRP-----SCSC 37  
 DB 4 ERYTYA--ELKVAANSRQHRKPRGPNSSIVIOEITISDFSPQNPQEHPICRNCPG 61  
 QY 38 -----LVATILGLITAVL--SVLLYQWILCOGSNY--STCASCPCSPDRMKYGNH 85  
 DB 62 KGFPPSPPEKLITAGLIGLIFLYAVVITVATPYINTLSSAQPCPHCKEMISTYSHN 121  
 QY 86 CYFYSVEEKWNSSLEPCCLARDSHLVITDQMSLLQVFLSEAFQWIG-LRNNSG--WR 142  
 DB 122 CYFIMGRKSMNDSLVSCISKNCSLYIDSEEDFLOSL--SLISWTGLRKGRGPVW 179  
 QY 143 WEDGSPINFRISNSFYQ-----TCGAINKNGLOASSCEVPLHYCK 185  
 DB 180 WKEDS-----IFRPKIAELHDECNAMMSASGILTADNCTTLHPYLCK 222

RESULT 10

054872 ID 054872 PRELIMINARY; PRT; 231 AA.

AC 054872;  
 DT 01-JUN-1998 (TREMBLrel. 06, Created)  
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE NATURAL KILLER CELL PROTEIN GROUP 2-A (FRAGMENT).  
 GN NKG2A.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=F344;  
 RX MEDLINE=98180346; Pubmed=9521051;  
 RA Berg S.F., Dissen E., Westgaard I.H., Fossum S.;  
 RT "Molecular characterization of two genes in the rat homologous to  
 human NKG2.";  
 RL Eur. J. Immunol. 28:444-450(1998).  
 DR EMBL; AF021350; AAC40050.1; -  
 DR InterPro: IPR001304; lectin\_c.  
 DR Pfam: PF00059; lectin\_c; 1.  
 DR SMART; SM00034; CLECT; 1.  
 DR PROSITE; PS50041; C\_TYPE\_LECTIN\_2; 1.  
 DR NON\_TER 1  
 FT 1  
 SQ SEQUENCE 231 AA; 26335 MW; FF2AB6D33EFZCE99 CRC64;

Query Match 20.5%; Score 210; DB 11; Length 231;  
 Best Local Similarity 29.0%; Pred. No. 4.3e-15;

Matches 54; Conservative 25; Mismatches 81; Indels 26; Gaps 5;

QY 24 PQQKSSSSKPCSC-----LVATILGLITAVLSVL-----YQWILCOGSNY 66  
 DB 43 PSQQRICRCDCKHKGFPSPPEKLITAGLISFLYIAVVAVITVATPYETKQINSS 102  
 QY 67 ST-----CASCPCSPDRMKYGNHCYFVSVEEKWNSSLEPCCLARDSHLVITDQMSLL 122  
 DB 103 MTRTYQARPCIRCDPMWISHNCTIYISVERKSMNDSGLTSCISKNSLHIDSEEOAFL 162

QY 123 QVFLSEAFQWIGLRNNS---GWRWEDGSPINFRISNSFVOTCGAINKNGLOASSCEVP 179  
 DB 163 QSF--SLVSWGCFRRKSNQSPVWENGSTFRKRTIEMLHDEYNIMMSTSGLAENCTIL 220

QY 180 LHGYCK 185  
 DB 221 HPYCK 226

RESULT 11

095MT5 ID 095MT5 PRELIMINARY; PRT; 233 AA.

AC 095MT5;  
 DT 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE NKG2A.  
 GN NKG2A.  
 OS Pan troglodytes (Chimpanzee).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Pan.  
 OX NCBI\_TaxID=9598;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Shum B.P., Flodin L.R., Muir D.G.;  
 RT "CD94 and NKG2 Genes in Human and Common Chimpanzee."  
 RL Submitted (FEB-2001) to the EMBL/Genbank/DBD databases.  
 DR EMBL; AF350005; AAK83792.1; -  
 SQ SEQUENCE 233 AA; 26231 MW; A993D9648000CC84 CRC64;

Query Match 19.8%; Score 203; DB 6; Length 233;  
 Best Local Similarity 28.8%; Pred. No. 2.6e-14;

Matches 57; Conservative 34; Mismatches 87; Indels 20; Gaps 7;

QY 5 VYVSLMELPTAQ--AONDYGPQKSSSKPSCCLVATILGLITAVL-----SVLLYQW 58  
 DB 38 IYVALNLQKASQDQENDKTYHCKDLPSAP--EKIIVIGLIGLILMASVYTIYVVS 95  
 QY 59 ILCOGSNYST-----CASCPCSPDRMKYGNHCYFVSVEEKWNSSLEPCCLARDSHLL 111  
 DB 96 TLIQHNHNSLNTPTQKARHCCHPEEWITNSCYLIKERTWESILACTSKNSGLL 155  
 QY 112 VITDQMSLLQVFLSEAFQWIGL-RNNSGWRWEDGSPINFR--ISSNFVOTCGAINK 168  
 DB 156 SIDNEEMKFLSIISPS--WIGVFRNSSHPWYTINGLAFRHEIKSDNAELNCAYLOY 213  
 QY 169 NGLQASSCEVPLHYCKR 186  
 DB 214 NGLKSAQCGSSITTYHCKR 231

RESULT 12

09MZK3 ID 09MZK3 PRELIMINARY; PRT; 231 AA.

AC 09MZK3;  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE NKG2-C.  
 OS Macaca mulatta (Rhesus macaque).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopithecoidea; Macaca.  
 OX NCBI\_TaxID=9544;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20322487; Pubmed=10866118;  
 RA Laibonte M.L., Levy D.B., Letvin N.L.;  
 RT "Characterization of rhesus monkey CD94/NKG2 family members and  
 identification of novel transmembrane-deleted forms of NKG2-A, B, C,  
 and D.";  
 RL Immunogenetics 51:496-499(2000).



RT splicing of 5' exons in rhesus monkey decidua.",  
 RL Immunogenetics 53:59-73(2001).  
 DR EXML: AF294889; AAC34501.1; -  
 DR HSSP: P06734; IHLI.  
 DR InterPro: IPR001304; lectin-c.  
 DR Pfam: PF000050; lectin-c; 1.  
 DR SMART: SM00034; CLECT\_1.  
 DR PROSITE, PSS004; C\_TYPE, LECTIN-2; 1.  
 DR PROSITE, PSS004; C\_TYPE, LECTIN-2; 1.  
 SO SEQUENCE 211 AA; 26168 MW; D53C0F9126C41DB3 CRC64;

Query Match	19.5%;	Score 199.5;	DB 6;	Length 231;
Best Local Similarity	28.3%;	Pred. No. 6	2e-14;	
Matches	56;	Conservative	33;	Mismatches 92;
				Indels 17;
				Gaps 6;

[illegible]

Search completed: September 9, 2002, 15:03:39  
Job time: 233 sec